



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Weiner, Joel H.
Turner, Raymond J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
SECRETION

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Medlen & Carroll, LLP
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(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: United States of America
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/085,761
(B) FILING DATE: 28-MAY-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Carroll, Peter G.
(B) REGISTRATION NUMBER: 32,837
(C) REFERENCE/DOCKET NUMBER: UALB-03356

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 705-8410
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Arg	Leu	Cys	Leu	Ile	Ile	Ile	Tyr	His	Arg	Gly	Thr	Cys	Met	Gly
1				5					10					15	
Gly	Ile	Ser	Ile	Trp	Gln	Leu	Leu	Ile	Ile	Ala	Val	Ile	Val	Val	Leu
				20				25					30		
Leu	Phe	Gly	Thr	Lys	Lys	Leu	Gly	Ser	Ile	Gly	Ser	Asp	Leu	Gly	Ala
				35			40					45			

Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro Lys Gln
 50 55 60
 Asp Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile Ala Asp
 65 70 75 80
 Lys Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Thr Glu Asp Ala Lys
 85 90 95
 Arg His Asp Lys Glu Gln Gly Val Asn Pro Cys Leu Ile Ser Val Leu
 100 105 110
 Ala Asn Leu Leu Leu Val Phe Ile Ile Gly Leu Val Val Leu Gly Pro
 115 120 125
 Gln Arg Leu Pro Val Ala Val Lys Thr Val Ala Gly Trp Ile Arg Ala
 130 135 140
 Leu Arg Ser Leu Ala Thr Thr Val Gln Asn Glu Leu Thr Gln Glu Leu
 145 150 155 160
 Lys Leu Gln Glu Phe Gln Asp Ser Leu Lys Lys Val Glu Lys Ala Ser
 165 170 175
 Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala Ser Met Asp Glu Leu Arg
 180 185 190
 Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr Val Ala Asn Asp Pro Glu
 195 200 205
 Lys Ala Ser Asp Glu Ala His Thr Ile His Asn Pro Val Val Lys Asp
 210 215 220
 Asn Glu Ala Ala His Glu Gly Val Thr Pro Ala Ala Ala Gln Thr Gln
 225 230 235 240
 Ala Ser Ser Pro Glu Gln Lys Pro Glu Thr Thr Pro Glu Pro Val Val
 245 250 255
 Lys Pro Ala Ala Asp Ala Glu Pro Lys Thr Ala Ala Pro Ser Pro Ser
 260 265 270
 Ser Ser Asp Lys Pro
 275

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Lys Lys Ser Ile Phe Arg Ala Lys Phe Phe Leu Phe Tyr Arg
 1 5 10 15
 Thr Glu Phe Ile Met Phe Gly Leu Ser Pro Ala Gln Leu Ile Ile Leu
 20 25 30

Leu Val Val Ile Leu Leu Ile Phe Gly Thr Lys Lys Leu Arg Asn Ala
 35 40 45
 Gly Ser Asp Leu Gly Ala Ala Val Lys Gly Phe Lys Lys Ala Met Lys
 50 55 60
 Glu Asp Glu Lys Val Lys Asp Ala Glu Phe Lys Ser Ile Asp Asn Glu
 65 70 75 80
 Thr Ala Ser Ala Lys Lys Gly Lys Tyr Lys Arg Glu Arg Asn Arg Leu
 85 90 95
 Asn Pro Cys Leu Ile Leu Val Phe Gln Asn Leu Phe Tyr Xaa Met Val
 100 105 110
 Leu Gly Leu Val Val Leu Gly Pro Lys Arg Leu Pro Ile Ala Ile Arg
 115 120 125
 Thr Val Met Asp Trp Val Lys Thr Ile Arg Gly Leu Ala Ala Asn Val
 130 135 140
 Gln Asn Glu Leu Lys Gln Glu Leu Lys Leu Gln Glu Leu Gln Asp Ser
 145 150 155 160
 Ile Lys Lys Ala Glu Ser Leu Asn Leu Gln Ala Leu Ser Pro Glu Leu
 165 170 175
 Ser Lys Thr Val Glu Glu Leu Lys Ala Gln Ala Asp Lys Met Lys Ala
 180 185 190
 Glu Leu Glu Asp Lys Ala Ala Gln Ala Gly Thr Thr Val Glu Asp Gln
 195 200 205
 Ile Lys Glu Ile Lys Ser Ala Ala Glu Asn Ala Glu Lys Ser Gln Asn
 210 215 220
 Ala Ile Ser Val Glu Glu Ala Ala Glu Thr Leu Ser Glu Ala Glu Arg
 225 230 235 240
 Thr Pro Thr Asp Leu Thr Ala Leu Glu Thr His Glu Lys Val Glu Leu
 245 250 255
 Asn Thr His Leu Ser Ser Tyr Tyr Pro Pro Asp Asp Ile Glu Ile Ala
 260 265 270
 Pro Ala Ser Lys Ser Gln Ser Ser Lys Thr Lys Ser
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGTCCTGCAG AATGAAGGGT GATTTATGTG ATTTGCATCA CTTTGGTGG GTAAATTTAT

60

GCAACGCATT	TGCGTCATGG	TGATGAGTAT	CACGAAAAAA	TGTTAAACCC	TTCGGTAAAG	120
TGTCTTTTTG	CTTCTTCTGA	CTAAACCGAT	TCACAGAGGA	GTTGTATATG	TCCAAGTCTG	180
ATGTTTTTCA	TCTCGGCCTC	ACTAAAAACG	ATTTACAAGG	GGCTACGCTT	GCCATCGTCC	240
CTGGCGACCC	GGATCGTGTG	GAAAAGATCG	CCGCGCTGAT	GGATAAGCCG	GTTAAGCTGG	300
CATCTCACCG	CGAATTCACT	ACCTGGCGTG	CAGAGCTGGA	TGGTAAACCT	GTTATCGTCT	360
GCTCTACCGG	TATCGGCGGC	CCGTCTACCT	CTATTGCTGT	TGAAGAGCTG	GCACAGCTGG	420
GCATTGCGAC	CTTCTGCGT	ATCGGTACAA	CGGGCGCTAT	TCAGCCGCAT	ATTAATGTGG	480
GTGATGTCCT	GGTTACCACG	GCGTCTGTCC	GTCTGGATGG	CGCGAGCCTG	CACTTCGCAC	540
CGCTGGAATT	CCCGGCTGTC	GCTGATTTTC	AATGTACGAC	TGCGCTGGTT	GAAGCTGCGA	600
AATCCATTGG	CGCGACAAC	CACGTTGGCG	TGACAGCTTC	TTCTGATACC	TTCTACCCAG	660
GTCAGGAACG	TTACGATACT	TACTCTGGTC	GCGTAGTTTC	TCACTTTAAA	GGTTCTATGG	720
AAGAGTGGCA	GGCGATGGGC	GTAATGAACT	ATGAAATGGA	ATCTGCAACC	CTGCTGACCA	780
TGTGTGCAAG	TCAGGGCCTG	CGTGCCGGTA	TGGTAGCGGG	TGTTATCGTT	AACCGCACCC	840
AGCAAGAGAT	CCCGAATGCT	GAGACGATGA	AACAAACCGA	AAGCCATGCG	GTGAAAATCG	900
TGGTGGAAGC	GGCGCGTCGT	CTGCTGTAAT	TCTCTTCTCC	TGTCTGAAGG	CCGACGCGTT	960
CGGCCTTTTG	TATTTTTGCG	TAGCGCCTCG	CAGGAAATGC	CTTTCCAAC	GGACGTTTGT	1020
ACAGCACAAT	TCTATTTTGT	GCGGGTAAGT	TGTTGCGTCA	GGAGGCGTTG	TGGATTTCTC	1080
AATCATGGTT	TACGCAGTTA	TTGCGTTGGT	GGGTGTGGCA	ATTGGCTGGC	TGTTTGCCAG	1140
TTATCAACAT	GCGCAGCAAA	AAGCCGAGCA	ATTAGCTGAA	CGTGAAGAGA	TGGTCGCGGA	1200
GTTAAGCGCG	GCAAAACAAC	AAATTACCCA	AAGCGAGCAC	TGGCGTGCAG	AGTGCGAGTT	1260
ACTCAATAAC	GAAGTGCGCA	GCCTGCAAAG	TATTAACACC	TCTCTGGAGG	CCGATCTGCG	1320
TGAAGTAACC	ACGCGGATGG	AAGCCGCACA	GCAACATGCT	GACGATAAAA	TTCGCCAGAT	1380
GATTAACAGC	GAGCAGCGCC	TCAGTGAGCA	GTTTGAAAAC	CTCGCCAACC	GTATTTTTGA	1440
GCACAGCAAT	CGCCGGGTTG	ATGAGCAAAA	CCGTCAGAGT	CTGAACAGCC	TGTTGTCGCC	1500
GCTACGTGAA	CAACTGGACG	GTTTCCGCCG	TCAGGTTTTC	GACAGCTTCG	GTAAAGAAGC	1560
ACAAGAACGC	CATACCCTGA	CCCACGAAAT	TCGCAATCTC	CAGCAACTCA	ACGCGCAAAT	1620
GGCCCAGGAA	GCGATCAACC	TGACGCGCGC	GCTGAAAGGC	GACAATAAAA	CCCAGGGCAA	1680
CTGGGGCGAG	GTAGTATTGA	CGCGGGTGCT	GGAGGCTTCC	GGTCTGCGTG	AAGGGTATGA	1740
ATATGAAACC	CAGGTCAGCA	TCGAAAATGA	CGCCCCTCTG	CGGATGCAGC	CGGATGTCAT	1800
CGTGCGCCTG	CCGCAGGGAA	AAGATGTGGT	GATCGACGCC	AAAATGACGC	TGGTCGCCTA	1860
TGAACGCTAT	TTTAACGCCG	AAGACGACTA	CACCCGCGAA	AGCGCGCTAC	AGGAACATAT	1920

CGCGTCGGTG	CGTAACCATA	TCCGTTTGCT	GGGACGCAAA	GATTATCAAC	AGCTGCCGGG	1980
GCTGCGAACT	CTGGATTACG	TGCTGATGTT	TATTCCCGTT	GAACCCGCTT	TTTTACTGGC	2040
GCTTGACCGC	CAGCCGGAGC	TGATCACCGA	AGCGTTGAAA	AACAACATCA	TGCTGGTTAG	2100
CCCGACTACG	CTGCTGGTGG	CGCTGCGCAC	TATCGCCAAC	CTGTGGCGTT	ATGAGCATCA	2160
AAGCCGCAAC	GCCCAGCAAA	TCGCCGATCG	TGCCAGCAAG	CTGTACGACA	AGATGCGTTT	2220
GTTTCATCGAT	GACATGTCCG	CGATTGGTCA	AAGTCTCGAC	AAAGCGCAGG	ATAATTATCG	2280
GCAGGCAATG	AAAAAACTCT	CTTCAGGGCG	CGGAAATGTG	CTGGCGCAGG	CAGAAGCGTT	2340
TCGCGGTTTA	GGAGTAGAAA	TTAAACGCGA	GATTAATCCG	GATTTGGCTG	AACAGGCGGT	2400
GAGCCAGGAT	GAAGAGTATC	GACTTCGGTC	GGTTCCGGAG	CAGCCGAATG	ATGAAGCTTA	2460
TCAACGCGAT	GATGAATATA	ATCAGCAGTC	GCGCTAGCCC	ATTGGGAGTA	GTTAAGCCGG	2520
GTAGAAATCT	AGGGCATCGA	CGCCCAATCT	GTTACACTTC	TGGAACAATT	TTTTGATGAG	2580
CAGGCATTGA	GATGGTGGAT	AAGTCACAAG	AAACGACGCA	CTTTGGTTTT	CAGACCGTCG	2640
CGAAGGAACA	AAAAGCGGAT	ATGGTCGCCC	ACGTTTTTCCA	TTCCGTGGCA	TCAAAATACG	2700
ATGTCATGAA	TGATTTGATG	TCATTTGGTA	TTCATCGTTT	GTGGAAGCGA	TTCACGATTG	2760
ATTGCAGCGG	CGTACGCCGT	GGGCAGACCG	TGCTGGATCT	GGCTGGTGGC	ACCGGCGACC	2820
TGACAGCGAA	ATTCTCCCGC	CTGGTCGGAG	AAACTGGCAA	AGTGGTCCTT	GCTGATATCA	2880
ATGAATCCAT	GCCCCAAAATG	GGCCGCGAGA	AGCTGCGTAA	TATCGGTGTG	ATTGGCAACG	2940
TTGAGTATGT	TCAGGCGAAC	GCTGAGGCGC	TGCCGTTCCC	GGATAACACC	TTTGATTGCA	3000
TCACCATTTT	GTTTGGTCTG	CGTAACGTCA	CCGACAAAGA	TAAAGCACTG	CGTTCAATGT	3060
ATCGCGTGCT	GAAACCCGGC	GGCCGCCTGC	TGGTGCTTGA	GTTCTCGAAG	CCAATTATCG	3120
AGCCGCTGAG	CAAAGCCTAT	GATGCATACT	CCTTCCATGT	GCTGCCGCGT	ATTGGCTCAC	3180
TGGTCGCGAA	CGACGCCGAC	AGCTACCGTT	ATCTGGCAGA	ATCCATCCGT	ATGCATCCCG	3240
ATCAGGATAC	CCTGAAAGCC	ATGATGCAGG	ATGCCGGATT	CGAAAGTGTC	GACTIONTACA	3300
ATCTGACGGC	AGGGGTTGTG	GCGCTGCATC	GTGGTTATAA	GTTCTGACAG	GAGACCGGAA	3360
ATGCCTTTTA	AACCTTTAGT	GACGGCAGGA	ATTGAAAGTC	TGCTCAACAC	CTTCCTGTAT	3420
CGCTCACCCG	CGCTGAAAAC	GGCCCGCTCG	CGTCTGCTGG	GTAAAGTATT	GCGCGTGGAG	3480
GTAAAGGCT	TTTCGACGTC	ATTGATTCTG	GTGTTACAGC	AACGCCAGGT	TGATGTACTG	3540
GGCGAATGGG	CAGGCGATGC	TGACTGCACC	GTTATCGCCT	ACGCCAGTGT	GTTGCCGAAA	3600
CTTCGCGATC	GCCAGCAGCT	TACCGCACTG	ATTCGCAGTG	GTGAGCTGGA	AGTGCAGGGC	3660
GATATTCAGG	TGGTGCAAAA	CTTCGTTGCG	CTGGCAGATC	TGGCAGAGTT	CGACCCTGCG	3720
GAAGTGCTGG	CCCCTTATAC	CGGTGATATC	GCCGCTGAAG	GAATCAGCAA	AGCCATGCGC	3780

GGAGGCGCAA	AGTTCCTGCA	TCACGGCATT	AAGCGCCAGC	AACGTTATGT	GGCGGAAGCC	3840
ATTACTGAAG	AGTGGCGTAT	GGCACCCGGT	CCGCTTGAAG	TGGCCTGGTT	TGCGGAAGAG	3900
ACGGCTGCCG	TCGAGCGTGC	TGTTGATGCC	CTGACCAAAC	GGCTGGAAAA	ACTGGAGGCT	3960
AAATGACGCC	AGGTGAAGTA	CGGCGCCTAT	ATTTTCATCAT	TCGCACTTTT	TTAAGCTACG	4020
GACTTGATGA	ACTGATCCCC	AAAATGCGTA	TCACCCTGCC	GCTACGGCTA	TGGCGATACT	4080
CATTATTCTG	GATGCCAAAT	CGGCATAAAG	ACAAACTTTT	AGGTGAGCGA	CTACGACTGG	4140
CCCTGCAAGA	ACTGGGGCCG	GTTTGGATCA	AGTTCGGGCA	AATGTTATCA	ACCCGCCGCG	4200
ATCTTTTTTC	ACCGCATATT	GCCGATCAGC	TGGCGTTATT	GCAGGACAAA	GTTGCTCCGT	4260
TTGATGGCAA	GCTGGCGAAG	CAGCAGATTG	AAGCTGCAAT	GGGCGGCTTG	CCGGTAGAAG	4320
CGTGGTTTTGA	CGATTTTGAA	ATCAAGCCGC	TGGCTTCTGC	TTCTATCGCC	CAGGTTTATA	4380
CCGCGCGATT	GAAATCGAAT	GGTAAAGAGG	TGGTGATTAA	AGTCATCCGC	CCGGATATTT	4440
TGCCGGTTAT	TAAAGCGGAT	CTGAAACTTA	TCTACCGTCT	GGCTCGCTGG	GTGCCGCGTT	4500
TGCTGCCGGA	TGGTCGCCGT	CTGCGCCCAA	CCGAAGTGGT	GCGCGAGTAC	GAAAAGACAT	4560
TGATTGATGA	ACTGAATTTG	CTGCGGGAAT	CTGCCAACGC	CATTCAGCTT	CGGCGCAATT	4620
TTGAAGACAG	CCCGATGCTC	TACATCCCGG	AAGTTTACCC	TGACTATTGT	AGTGAAGGGA	4680
TGATGGTGAT	GGAGCGCATT	TACGGCATTG	CGGTGTCTGA	TGTTGCGGCG	CTGGAGAAAA	4740
ACGGCACTAA	CATGAAATTG	CTGGCGGAAC	GCGGCGTGCA	GGTGTTCCTC	ACTCAGGTCT	4800
TTGCGGACAG	CTTTTTCCAT	GCCGATATGC	ACCCTGGCAA	CATCTTCGTA	AGCTATGAAC	4860
ACCCGGAAAA	CCCGAAATAT	ATCGGCATTG	ATTGCGGGAT	TGTTGGCTCG	CTAAACAAAG	4920
AAGATAAACG	CTATCTGGCA	GAAAACTTTA	TCGCCTTCTT	TAATCGCGAC	TATCGCAAAG	4980
TGGCAGAGCT	ACACGTCGAT	TCTGGCTGGG	TGCCACCAGA	TACCAACGTT	GAAGAGTTCTG	5040
AATTTGCCAT	TCGTACGGTC	TGTGAACCTA	TCTTTGAGAA	ACCGCTGGCC	GAAATTTCTG	5100
TTGGACATGT	ACTGTTAAAT	CTGTTTAATA	CGGCGCGTCG	CTTCAATATG	GAAGTGCAGC	5160
CGCAACTGGT	GTTACTCCAG	AAAACCCTGC	TCTACGTCGA	AGGGGTAGGA	CGCCAGCTTT	5220
ATCCGCAACT	CGATTTATGG	AAAACGGCGA	AGCCTTTTCT	GGAGTCGTGG	ATTAAAGATC	5280
AGGTCGGTAT	TCCTGCGCTG	GTGAGAGCAT	TTAAAGAAAA	AGCGCCGTTT	TGGGTCGAAA	5340
AAATGCCAGA	ACTGCCTGAA	TTGGTTTACG	ACAGTTTGCG	CCAGGGCAAG	TATTTACAGC	5400
ACAGTGTTGA	TAAGATTGCC	CGCGAGCTTC	AGTCAAATCA	TGTACGTCAG	GGACAATCGC	5460
GTTATTTTCT	CGGAATTGGC	GCTACGTTAG	TATTAAGTGG	CACATTCTTG	TTGGTCAGCC	5520
GACCTGAATG	GGGGCTGATG	CCCGGCTGGT	TAATGGCAGG	TGGTCTGATC	GCCTGGTTTTG	5580
TCGGTTGGCG	CAAAACACGC	TGATTTTTTC	ATCGCTCAAG	GCGGGCCGTG	TAACGTATAA	5640

TGCGGCTTTG	TTTAATCATC	ATCTACCACA	GAGGAACATG	TATGGGTGGT	ATCAGTATTT	5700
GGCAGTTATT	GATTATTGCC	GTCATCGTTG	TACTGCTTTT	TGGCACCAAA	AAGCTCGGCT	5760
CCATCGGTTC	CGATCTTGGT	GCGTCGATCA	AAGGCTTTAA	AAAAGCAATG	AGCGATGATG	5820
AACCAAAGCA	GGATAAAACC	AGTCAGGATG	CTGATTTTAC	TGCGAAAACT	ATCGCCGATA	5880
AGCAGGCGGA	TACGAATCAG	GAACAGGCTA	AAACAGAAGA	CGCGAAGCGC	CACGATAAAG	5940
AGCAGGTGAA	TCCGTGTTTG	ATATCGGTTT	TAGCGAACTT	GCTATTGGTG	TTCATCATCG	6000
GCCTCGTCGT	TCTGGGGCCG	CAACGACTGC	CTGTGGCGGT	AAAAACGGTA	GCGGGCTGGA	6060
TTCGCGCGTT	GCGTTCACTG	GCGACAACGG	TGCAGAACGA	ACTGACCCAG	GAGTTAAAC	6120
TCCAGGAGTT	TCAGGACAGT	CTGAAAAGG	TTGAAAAGGC	GAGCCTCACT	AACCTGACGC	6180
CCGAACTGAA	AGCGTCGATG	GATGAACTAC	GCCAGGCCGC	GGAGTCGATG	AAGCGTTCCT	6240
ACGTTGCAAA	CGATCCTGAA	AAGGCGAGCG	ATGAAGCGCA	CACCATCCAT	AACCCGGTGG	6300
TGAAAGATAA	TGAAGCTGCG	CATGAGGGCG	TAACGCCTGC	CGCTGCACAA	ACGCAGGCCA	6360
GTTTCGCCGA	ACAGAAGCCA	GAAACCACGC	CAGAGCCGGT	GGTAAAACCT	GCTGCGGACG	6420
CTGAACCGAA	AACCGCTGCA	CCTTCCCCTT	CGTCGAGTGA	TAAACCGTAA	ACATGTCTGT	6480
AGAAGATACT	CAACCGCTTA	TCACGCATCT	GATTGAGCTG	CGTAAGCGTC	TGCTGAACTG	6540
CATTATCGCG	GTGATCGTGA	TATTCCTGTG	TCTGGTCTAT	TTCGCCAATG	ACATCTATCA	6600
CCTGGTATCC	GCGCCATTGA	TCAAGCAGTT	GCCGCAAGGT	TCAACGATGA	TCGCCACCGA	6660
CGTGGCCTCG	CCGTTCTTTA	CGCCGATCAA	GCTGACCTTT	ATGGTGTGCG	TGATTCTGTC	6720
AGCGCCGGTG	ATTCTCTATC	AGGTGTGGGC	ATTTATCGCC	CCAGCGCTGT	ATAAGCATGA	6780
ACGTCGCCTG	GTGGTGCCGC	TGCTGGTTTC	CAGCTCTCTG	CTGTTTTATA	TCGGCATGGC	6840
ATTCGCCTAC	TTTGTGGTCT	TTCCGCTGGC	ATTTGGCTTC	CTTGCCAATA	CCGCGCCGGA	6900
AGGGGTGCAG	GTATCCACCG	ACATCGCCAG	CTATTTAAGC	TTCGTTATGG	CGCTGTTTAT	6960
GGCGTTTGGT	GTCTCCTTTG	AAGTGCCGGT	AGCAATTGTG	CTGCTGTGCT	GGATGGGGAT	7020
TACCTCGCCA	GAAGACTTAC	GCAAAAAACG	CCCGTATGTG	CTGGTTGGTG	CATTTCGTTGT	7080
CGGGATGTTG	CTGACGCCGC	CGGATGTCTT	CTCGCAAACG	CTGTTGGCGA	TCCCGATGTA	7140
CTGTCTGTTT	GAAATCGGTG	TCTTCTTCTC	ACGCTTTTAC	GTTGGTAAAG	GGCGAAATCG	7200
GGAAGAGGAA	AACGACGCTG	AAGCAGAAAG	CGAAAAAACT	GAAGAATAAA	TTCAACCGCC	7260
CGTCAGGGCG	GTTGTCATAT	GGAGTACAGG	ATGTTTGATA	TCGGCGTTAA	TTTGACCAGT	7320
TCGCAATTTG	CGAAAGACCG	TGATGATGTT	GTAGCGTGCG	CTTTTGACGC	GGGAGTTAAT	7380
GGGCTACTCA	TCACCGGCAC	TAACCTGCGT	GAAAGCCAGC	AGGCGCAAAA	GCTGGCGCGT	7440
CAGTATTCGT	CCTGTTGGTC	AACGGCGGGC	GTACATCCTC	ACGACAGCAG	CCAGTGGCAA	7500

GCTGCGACTG	AAGAAGCGAT	TATTGAGCTG	GCCGCGCAGC	CAGAAGTGGT	GGCGATTGGT	7560
GAATGTGGTC	TCGACTTTAA	CCGCAACTTT	TCGACGCCGG	AAGAGCAGGA	ACGCGCTTTT	7620
GTTGCCCAGC	TACGCATTGC	CGCAGATTTA	AACATGCCGG	TATTTATGCA	CTGTCGCGAT	7680
CCCCACGAGC	GGTTTATGAC	ATTGCTGGAG	CCGTGGCTGG	ATAAACTGCC	TGGTGC GGTT	7740
CTTCATTGCT	TTACCGGCAC	ACGCGAAGAG	ATGCAGGCGT	GCGTGGCGCA	TGGAATTTAT	7800
ATCGGCATTA	CCGGTTGGGT	TTGCGATGAA	CGACGCGGAC	TGGAGCTGCG	GGAACTTTTG	7860
CCGTTGATTC	CGGCGGAAAA	ATTACTGATC	GAAACTGATG	CGCCGTATCT	GCTCCCTCGC	7920
GATCTCACGC	CAAAGCCATC	ATCCCGGCGC	AACGAGCCAG	CCCATCTGCC	CCATATTTTG	7980
CAACGTATTG	CGCACTGGCG	TGGAGAAGAT	GCCGCATGGC	TGGCTGCCAC	CACGGATGCT	8040
AATGTCAAAA	CACTGTTTGG	GATTGCGTTT	TAGAGTTTGC	GGAACTCGGT	ATTCTTCACA	8100
CTGTGCTTAA	TCTCTTTATT	AATAAGATTA	AGCAATAGCA	TGGAGCGAGC	CTCACCATCG	8160
GGTTCGGTGA	AAATGGCCTG	AAAGCCTTCG	AACGCGCCTT	CGGTAATAAT	CACCTTATCA	8220
CCCGGATAAG	GGGTTGCCGG	ATCGACAATG	TCTTTCGGTT	TATATACCGA	TAGCTGATGA	8280
ATAACCGCCG	ATGGGACTAT	CGCTGGCGAC	GCGCCAAAGC	GCACGAAGTG	GCTGACACCG	8340
CGGGTCGCGT	TGATAGTCGT	GGTATGAATC	ACTTCTGGGT	CAAATTCAC	AAACAGGTAG	8400
TTGGGGAACA	ATGGCTCACT	GACTGCAGTA	CGTTTTCCAC	GCACGATTTT	TTCCAGGGTG	8460
ATCATCGGTG	CCAGGCAATT	CACAGCCTGT	CTTTCGAGGT	GTTCTGGGC	ACGTTGAAGT	8520
TGCCC GCGCT	TGCAGTACAG	TAAATACCAG	GATTGCATAA	TGACTCTTAT	CCGTTTAATC	8580
GGGGCGCAAG	GATAGCAAAA	GCTTTACGCT	AAGTTAATTA	TATTCGCCGG	TTTGCGTTAT	8640
ACCGTCAGAG	TTCACGCTAA	TTTAACAAAT	TTACAGCATC	GCAAAGATGA	ACGCCGTATA	8700
ATGGGCGCAG	ATTAAGAGGC	TACAATGGAC	GCCATGAAAT	ATAACGATTT	ACGCGACTTC	8760
TTGACGCTGC	TTGAACAGCA	GGGTGAGCTA	AAACGTATCA	CGCTCCCGGT	GGATCCGCAT	8820
CTGGAAATCA	CTGAAATTGC	TGACCGCACT	TTGCGTGCCG	GTGGGCCTGC	GCTGTTGTTC	8880
GAAAACCCTA	AAGGCTACTC	AATGCCGGTG	CTGTGCAACC	TGTTCCGGTAC	GCCAAAGCGC	8940
GTGGCGATGG	GCATGGGGCA	GGAAGATGTT	TCGGCGCTGC	GTGAAGTTGG	TAAATTATTG	9000
GCGTTTCTGA	AAGAGCCGGA	GCCGCCAAAA	GGTTTCCGCG	ACCTGTTTGA	TAAACTGCCG	9060
CAGTTTAAGC	AAGTATTGAA	CATGCCGACA	AAGCGGCTGC	GTGGTGCGCC	CTGCCAACAA	9120
AAAATCGTCT	CTGGCGATGA	CGTCGATCTC	AATCGCATTTC	CCATTATGAC	CTGCTGGCCG	9180
GAAGATGCCG	CGCCGCTGAT	TACCTGGGGG	CTGACAGTGA	CGCGCGGCC	ACATAAAGAG	9240
CGGCAGAATC	TGGGCATTTA	TCGCCAGCAG	CTGATTGGTA	AAAACAACT	GATTATGCGC	9300
TGGCTGTCGC	ATCGCGGCGG	CGCGCTGGAT	TATCAGGAGT	GGTGTGCGGC	GCATCCGGGC	9360

GAACGTTTCC	CGGTTTCTGT	GGCGCTGGGT	GCCGATCCCG	CCACGATTCT	CGGTGCAGTC	9420
ACTCCCGTTC	CGGATACGCT	TTCAGAGTAT	GCGTTTGCCG	GATTGCTACG	TGGCACCAAG	9480
ACCGAAGTGG	TGAAGTGTAT	CTCCAATGAT	CTTGAAGTGC	CCGCCAGTGC	GGAGATTGTG	9540
CTGGAAGGGT	ATATCGAACA	AGGCGAAACT	GCGCCGGAAG	GGCCGTATGG	CGACCACACC	9600
GGTTACTATA	ATGAAGTCGA	TAGTTTCCCG	GTATTTACCG	TGACGCATAT	TACCCAGCGT	9660
GAAGATGCGA	TTTACCATTG	CACCTATACC	GGGCGTCCGC	CAGATGAGCC	CGCGGTGCTG	9720
GGTGTGCGAC	TGAACGAAGT	GTTTGTGCCG	ATTCTGCAAA	AACAGTTCCC	GGAAATTGTC	9780
GATTTTTACC	TGCCGCCGGA	AGGCTGCTCT	TATCGCCTGG	CGGTAGTGAC	AATCAAAAAA	9840
CAGTACGCCG	GACACGCGAA	GCGCGTCATG	ATGGGCGTCT	GGTCGTTCTT	ACGCCAGTTT	9900
ATGTACACTA	AATTTGTGAT	CGTTTGCGAT	GATGACGTTA	ACGCACGCGA	CTGGAACGAT	9960
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AACGGTAAAA	GCGCCTGATG	CGCGTTTGTT	TTGCCCTATT	TATCGATCCG	ACAGAGAAAG	10260
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GTGATGGATG	AGCGCGACAA	ACGTCCGTTC	TCAATGGCTT	CGACGCCGGA	TGAAAAAGGG	10440
TTTATCGAGC	TGCATATTGG	CGCTTCTGAA	ATCAACCTTT	ACGCGAAAGC	AGTCATGGAC	10500
CGCATCCTCA	AAGATCATCA	AATCGTGGTC	GACATTCCCC	ACGGAGAAGC	GTGGCTGCGC	10560
GATGATGAAG	AGCGTCCGAT	GATTTTGATT	GCGGGCGGCA	CCGGGTTCCTC	TTATGCCCGC	10620
TCGATTTTGC	TGACAGCGTT	GGCGCGTAAC	CCAAACCGTG	ATATCACCAT	TTACTGGGGC	10680
GGGCGTGAAG	AGCAGCATCT	GTATGATCTC	TGCGAGCTTG	AGGCGCTTTC	GTTGAAGCAT	10740
CCTGGTCTGC	AAGTGGTGCC	GGTGGTTGAA	CAACCGGAAG	CGGGCTGGCG	TGGGCGTACT	10800
GGCACCGTGT	TAACGGCGGT	ATTGCAGGAT	CACGGTACGC	TGGCAGAGCA	TGATATCTAT	10860
ATTGCCGGAC	GTTTTGAGAT	GGCGAAAATT	GCCCCGCGATC	TGTTTTGCAG	TGAGCGTAAT	10920
GCGCGGGAAG	ATCGCCTGTT	TGGCGATGCG	TTTGCAATTA	TCTGAGATAT	AAAAAACCC	10980
GCCCCTGACA	GGCGGGAAGA	ACGGCAACTA	AACTGTTATT	CAGTGGCATT	TAGATCTATG	11040
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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TCCATCGGTT CCGATCTTGG TCGTCGATC AAAGGCTTTA AAAAAGCAAT GAGCGATGAT	180
GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC TATCGCCGAT	240
AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACGCGAAGCG CCACGATAAA	300
GAGCAGGTGA ATCCGTGTTT GATATCGGTT TTAGCGAACT TGCTATTGGT GTTCATCATC	360
GGCCTCGTCG TTCTGGGGCC GCAACGACTG CCTGTGGCGG TAAAAACGGT AGCGGGCTGG	420
ATTGCGCGCT TGCCTTCACT GGCGACAACG GTGCAGAACG AACTGACCCA GGAGTTAAAA	480
CTCCAGGAGT TTCAGGACAG TCTGAAAAAG GTTGAAAAGG CGAGCCTCAC TAACCTGACG	540
CCCGAACTGA AAGCGTCGAT GGATGAACTA CGCCAGGCCG CGGAGTCGAT GAAGCGTTCC	600
TACGTTGCAA ACGATCCTGA AAAGGCGAGC GATGAAGCGC ACACCATCCA TAACCCGGTG	660
GTGAAAGATA ATGAAGCTGC GCATGAGGGC GTAACGCCTG CCGCTGCACA AACGCAGGCC	720
AGTTCGCCGG AACAGAAGCC AGAAACCACG CCAGAGCCGG TGGTAAAACC TGCTGCGGAC	780
GCTGAACCGA AAACCGCTGC ACCTTCCCCT TCGTCGAGTG ATAAACCGTA A	831

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTCTGTAG AAGATACTCA ACCGCTTATC ACGCATCTGA TTGAGCTGCG TAAGCGTCTG	60
CTGAACTGCA TTATCGCGGT GATCGTGATA TTCCTGTGTC TGGTCTATTT CGCCAATGAC	120
ATCTATCACC TGGTATCCGC GCCATTGATC AAGCAGTTGC CGCAAGGTTC AACGATGATC	180
GCCACCGACG TGGCCTCGCC GTTCTTTACG CCGATCAAGC TGACCTTTAT GGTGTGCTG	240
ATTCTGTCAG CGCCGGTGAT TCTCTATCAG GTGTGGGCAT TTATCGCCCC AGCGCTGTAT	300
AAGCATGAAC GTCGCCTGGT GGTGCCGCTG CTGGTTTCCA GCTCTCTGCT GTTTTATATC	360
GGCATGGCAT TCGCCTACTT TGTGGTCTTT CCGCTGGCAT TTGGCTTCCT TGCCAATACC	420
GCGCCGGAAG GGGTGCAGGT ATCCACCGAC ATCGCCAGCT ATTTAAGCTT CGTTATGGCG	480
CTGTTTATGG CGTTTGGTGT CTCCTTTGAA GTGCCGGTAG CAATTGTGCT GCTGTGCTGG	540

ATGGGGATTA CCTCGCCAGA AGACTTACGC AAAAAACGCC CGTATGTGCT GGTGTTGGTGCA	600
TTCGTTGTCTG GGATGTTGCT GACGCCGCCG GATGTCTTCT CGCAAACGCT GTTGGCGATC	660
CCGATGTACT GTCTGTTTGA AATCGGTGTC TTCTTCTCAC GCTTTTACGT TGGTAAAGGG	720
CGAAATCGGG AAGAGGAAAA CGACGCTGAA GCAGAAAGCG AAAAACTGA AGAATAAA	778

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGTACA GGATGTTTGA TATCGGCGTT AATTGACCA GTTCGCAATT TGCGAAAGAC	60
CGTGATGATG TTGTAGCGTG CGCTTTTGAC GCGGGAGTTA ATGGGCTACT CATCACCGGC	120
ACTAACCTGC GTGAAAGCCA GCAGGCGCAA AAGCTGGCGC GTCAGTATTC GTCCTGTTGG	180
TCAACGGCGG GCGTACATCC TCACGACAGC AGCCAGTGGC AAGCTGCGAC TGAAGAAGCG	240
ATTATTGAGC TGGCCGCGCA GCCAGAAGTG GTGGCGATTG GTGAATGTGG TCTCGACTTT	300
AACCGCAACT TTTGACGCC GGAAGAGCAG GAACGCGCTT TTGTTGCCCA GCTACGCATT	360
GCCGCAGATT TAAACATGCC GGTATTTATG CACTGTCGCG ATGCCACGA GCGGTTTATG	420
ACATTGCTGG AGCCGTGGCT GGATAAACTG CCTGGTGCGG TTCTTCATTG CTTTACCGGC	480
ACACGCGAAG AGATGCAGGC GTGCGTGGCG CATGGAATTT ATATCGGCAT TACCGGTTGG	540
GTTTGCGATG AACGACGCGG ACTGGAGCTG CGGGAACTTT TGCCGTTGAT TCCGGCGGAA	600
AAATTACTGA TCGAAACTGA TGCGCCGTAT CTGCTCCCTC GCGATCTCAC GCCAAAGCCA	660
TCATCCCGGC GCAACGAGCC AGCCCATCTG CCCCATATTT TGCAACGTAT TGCGCACTGG	720
CGTGGAGAAG ATGCCGCATG GCTGGCTGCC ACCACGGATG CTAATGTCAA AACACTGTTT	780
GGGATTGCGT TTTAG	795

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Val	Glu	Asp	Thr	Gln	Pro	Leu	Ile	Thr	His	Leu	Ile	Glu	Leu
1				5				10					15		

Arg Lys Arg Leu Leu Asn Cys Ile Ile Ala Val Ile Val Ile Phe Leu
 20 25 30
 Cys Leu Val Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ser Ala Pro
 35 40 45
 Leu Ile Lys Gln Leu Pro Gln Gly Ser Thr Met Ile Xaa Xaa Asp Val
 50 55 60
 Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu
 65 70 75 80
 Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala
 85 90 95
 Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val
 100 105 110
 Ser Ser Ser Leu Leu Phe Leu Tyr Arg His Ala Phe Ala Tyr Phe Val
 115 120 125
 Val Phe Pro Leu Ala Phe Gly Phe Leu Ala Asn Thr Ala Pro Glu Gly
 130 135 140
 Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala
 145 150 155 160
 Leu Phe Met Ala Phe Gly Val Ser Phe Glu Val Pro Val Ala Ile Val
 165 170 175
 Leu Leu Cys Trp Met Gly Ile Thr Ser Pro Glu Asp Leu Arg Lys Lys
 180 185 190
 Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly Met Leu Leu Thr
 195 200 205
 Pro Pro Asp Val Phe Ser Gln Thr Leu Leu Ala Ile Pro Met Tyr Cys
 210 215 220
 Leu Phe Glu Ile Gly Val Phe Phe Ser Arg Phe Tyr Val Gly Lys Gly
 225 230 235 240
 Arg Asn Arg Glu Glu Glu Asn Asp Ala Glu Ala Glu Ser Glu Lys Thr
 245 250 255
 Glu Glu

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Tyr Arg Met Phe Asp Ile Gly Val Asn Leu Thr Ser Ser Gln
 1 5 10 15

Phe Ala Lys Asp Arg Asp Asp Val Val Ala Cys Ala Phe Asp Ala Gly
20 25 30
Val Asn Gly Leu Leu Ile Thr Gly Thr Asn Leu Arg Glu Ser Gln Gln
35 40 45
Ala Gln Lys Leu Ala Arg Gln Tyr Ser Ser Cys Trp Ser Thr Ala Gly
50 55 60
Val His Pro His Asp Ser Ser Gln Trp Gln Ala Ala Thr Glu Glu Ala
65 70 75 80
Ile Ile Glu Leu Ala Ala Gln Pro Glu Val Val Ala Ile Gly Glu Cys
85 90 95
Gly Leu Asp Phe Asn Arg Asn Phe Ser Thr Pro Glu Glu Gln Glu Arg
100 105 110
Ala Phe Val Ala Gln Leu Arg Ile Ala Ala Asp Leu Asn Met Pro Val
115 120 125
Phe Met His Cys Arg Asp Ala His Glu Arg Phe Met Thr Leu Leu Glu
130 135 140
Pro Trp Leu Asp Lys Leu Pro Gly Ala Val Leu His Cys Phe Thr Gly
145 150 155 160
Thr Arg Glu Glu Met Gln Ala Cys Val Ala His Gly Ile Tyr Ile Gly
165 170 175
Ile Thr Gly Trp Val Cys Asp Glu Arg Arg Gly Leu Glu Leu Arg Glu
180 185 190
Leu Leu Pro Leu Ile Pro Ala Glu Lys Leu Leu Ile Glu Thr Asp Ala
195 200 205
Pro Tyr Leu Leu Pro Arg Asp Leu Thr Pro Lys Pro Ser Ser Arg Arg
210 215 220
Asn Glu Pro Ala His Leu Pro His Ile Leu Gln Arg Ile Ala His Trp
225 230 235 240
Arg Gly Glu Asp Ala Ala Trp Leu Ala Ala Thr Thr Asp Ala Asn Val
245 250 255
Lys Thr Leu Phe Gly Ile Ala Phe
260

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Pro Thr Ala Asn Leu Leu Leu Pro Ala Pro Pro Phe Val Pro
1 5 10 15

Ile Ser Asp Val Arg Arg Leu Gln Leu Pro Pro Arg Val Arg His Gln
 20 25 30
 Pro Arg Pro Cys Trp Lys Gly Val Glu Trp Gly Ser Ile Gln Thr Arg
 35 40 45
 Met Val Ser Ser Phe Val Ala Val Gly Ser Arg Thr Arg Arg Arg Asn
 50 55 60
 Val Ile Cys Ala Ser Leu Phe Gly Val Gly Ala Pro Glu Ala Leu Val
 65 70 75 80
 Ile Gly Val Val Ala Leu Leu Val Phe Gly Pro Lys Gly Leu Ala Glu
 85 90 95
 Val Ala Arg Asn Leu Gly Lys Thr Leu Arg Ala Phe Gln Pro Thr Ile
 100 105 110
 Arg Glu Leu Gln Asp Val Ser Arg Glu Phe Arg Ser Thr Leu Glu Arg
 115 120 125
 Glu Ile Gly Ile Asp Glu Val Ser Gln Ser Thr Asn Tyr Arg Pro Thr
 130 135 140
 Thr Met Asn Asn Asn Gln Gln Pro Ala Ala Asp Pro Asn Val Lys Pro
 145 150 155 160
 Glu Pro Ala Pro Tyr Thr Ser Glu Glu Leu Met Lys Val Thr Glu Glu
 165 170 175
 Gln Ile Ala Ala Ser Ala Ala Ala Ala Trp Asn Pro Gln Gln Pro Ala
 180 185 190
 Thr Ser Gln Gln Gln Glu Glu Ala Pro Thr Thr Pro Arg Ser Glu Asp
 195 200 205
 Ala Pro Thr Ser Gly Gly Ser Asp Gly Pro Ala Ala Pro Ala Arg Ala
 210 215 220
 Val Ser Asp Ser Asp Pro Asn Gln Val Asn Lys Ser Gln Lys Ala Glu
 225 230 235 240
 Gly Glu Arg

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Glu Ile Ser Ile Thr Lys Leu Leu Val Val Ala Ala Leu Val
 1 5 10 15
 Val Leu Leu Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu
 20 25 30

Gly Ala Ala Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala
35 40 45
Ala Ala Lys Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser
50 55 60
His Lys Glu
65

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Leu Thr Leu Val Met Gly Ala Ile Ala Ser Pro Trp Val Ser
1 5 10 15
Val Gly Thr Lys Leu Cys Tyr Ser Arg Leu Asn Glu Ser Phe Tyr Pro
20 25 30
Ser Asn Pro Leu Thr Ala Pro Asn Pro Met Asn Ile Phe Gly Ile Gly
35 40 45
Leu Pro Glu Leu Gly Leu Ile Phe Val Ile Ala Leu Leu Val Phe Gly
50 55 60
Pro Lys Lys Leu Pro Glu Val Gly Arg Ser Leu Gly Lys Ala Leu Arg
65 70 75 80
Gly Phe Gln Glu Ala Ser Lys Glu Phe Glu Thr Glu Leu Lys Arg Glu
85 90 95
Ala Gln Asn Leu Glu Lys Ser Val Gln Ile Lys Ala Glu Leu Glu Glu
100 105 110
Ser Lys Thr Pro Glu Ser Ser Ser Ser Ser Glu Lys Ala Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ala Met Ser Pro Trp His Trp Ala Ile Val Ala Leu Val Val
1 5 10 15
Val Ile Leu Phe Gly Ser Lys Lys Leu Pro Asp Ala Ala Arg Gly Leu
20 25 30

Gly Arg Ser Leu Arg Ile Phe Lys Ser Glu Val Lys Glu Met Gln Asn
 35 40 45
 Asp Asn Ser Thr Pro Ala Pro Thr Ala Gln Ser Ala Pro Pro Pro Gln
 50 55 60
 Ser Ala Pro Ala Glu Leu Pro Val Ala Asp Thr Thr Thr Ala Pro Val
 65 70 75 80
 Thr Pro Pro Ala Pro Val Gln Pro Gln Ser Gln His Thr Glu Pro Lys
 85 90 95
 Ser Ala

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Met Gly Ile Ser Val Trp Gln Leu Leu Ile Ile Leu Leu Ile Val
 1 5 10 15
 Val Met Leu Phe Gly Thr Lys Arg Leu Arg Gly Leu Gly Ser Asp Leu
 20 25 30
 Gly Ser Ala Ile Asn Gly Phe Arg Lys Ser Val Ser Asp Gly Glu Thr
 35 40 45
 Thr Thr Gln Ala Glu Ala Ser Ser Arg Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ser Leu Ser Pro Trp His Trp Val Val Leu Val Val Val Val
 1 5 10 15
 Val Leu Leu Phe Gly Ala Lys Lys Leu Pro Asp Ala Ala Arg Ser Leu
 20 25 30
 Gly Lys Ser Met Arg Ile Phe Lys Ser Glu Leu Arg Glu Met Gln Thr
 35 40 45
 Glu Asn Gln Ala Gln Ala Ser Ala Leu Glu Thr Pro Met Gln Asn Pro
 50 55 60

Thr Val Val Gln Ser Gln Arg Val Val Pro Pro Trp Ser Thr Glu Gln
65 70 75 80

Asp His Thr Glu Ala Arg Pro Ala
85

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val
1 5 10 15
Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly
20 25 30
Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu
35 40 45
Glu Glu Ala Lys Asn Glu Pro Lys Thr Leu Asp Ala Gln Ala Thr Gln
50 55 60
Thr Lys Val His Glu Ser Ser Glu Ile Lys Ser Lys Gln Glu Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Lys Lys Ser Ile Phe Arg Ala Lys Phe Phe Leu Phe Tyr Arg
1 5 10 15
Thr Glu Phe Ile Met Phe Gly Leu Ser Pro Ala Gln Leu Ile Ile Leu
20 25 30
Leu Val Val Ile Leu Leu Ile Phe Gly Thr Lys Lys Leu Arg Asn Ala
35 40 45
Gly Ser Asp Leu Gly Ala Ala Val Lys Gly Phe Lys Lys Ala Met Lys
50 55 60
Glu Asp Glu Lys Val Lys Asp Ala Glu Phe Lys Ser Ile Asp Asn Glu
65 70 75 80
Thr Ala Ser Ala Lys Lys Gly Lys Tyr Lys Arg Glu Arg Asn Arg Leu
85 90 95

Asn Pro Cys Leu Ile Leu Val Phe Gln Asn Leu Phe Tyr
 100 105

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Pro Ile Gly Pro Gly Ser Leu Ala Val Ile Ala Ile Val Ala Leu
 1 5 10 15
 Ile Ile Phe Gly Pro Lys Lys Leu Pro Glu Leu Gly Lys Ala Ala Gly
 20 25 30
 Asp Thr Leu Arg Glu Phe Lys Asn Ala Thr Lys Gly Leu Thr Ser Asp
 35 40 45
 Glu Glu Glu Lys Lys Lys Glu Asp Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Phe Gly Gly Ile Ser Ile Trp Gln Leu Leu Ile Ile Leu Leu
 1 5 10 15
 Ile Val Val Met Leu Phe Gly Thr Lys Arg Leu Lys Ser Leu Gly Ser
 20 25 30
 Asp Leu Gly Asp Ala Ile Lys Gly Phe Arg Lys Ser Met Asp Asn Glu
 35 40 45
 Glu Asn Lys Ala Pro Pro Val Glu Glu Gln Lys Gly Gln Asp His Arg
 50 55 60
 Gly Pro Gly Pro Gln Gly Arg Gly Thr Gly Gln Glu Arg Leu Ser Met
 65 70 75 80
 Phe Asp Ile Gly Phe Ser Glu Leu Leu Leu Val Gly Leu Val Ala Leu
 85 90 95
 Leu Val Leu Gly Pro Glu Arg Leu Pro Val Ala Ala Arg Met Ala Gly
 100 105 110
 Leu Trp Ile Gly Arg Leu Lys Arg Ser Phe Asn Thr Leu Lys Thr Glu
 115 120 125

Val	Glu	Arg	Glu	Ile	Gly	Ala	Asp	Glu	Ile	Arg	Arg	Gln	Leu	His	Asn
130						135					140				
Glu	Arg	Ile	Leu	Glu	Leu	Glu	Arg	Glu	Met	Lys	Gln	Ser	Leu	Gln	Pro
145					150					155					160
Pro	Ala	Pro	Ser	Ala	Pro	Asp	Glu	Thr	Ala	Ala	Ser	Pro	Ala	Thr	Pro
				165					170					175	
Pro	Gln	Pro	Ala	Ser	Pro	Ala	Ala	His	Ser	Asp	Lys	Thr	Pro	Ser	Pro
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr	Glu	His	Leu	Glu	Glu	Leu	Arg	Gln	Arg	Thr	Val	Phe	Val	Phe	Ile
1				5					10					15	
Phe	Phe	Leu	Leu	Ala	Ala	Thr	Ile	Ser	Phe	Thr	Gln	Ile	Lys	Ile	Ile
		20						25					30		
Val	Glu	Ile	Phe	Gln	Ala	Pro	Ala	Ile	Gly	Ile	Lys	Phe	Leu	Gln	Leu
		35					40					45			
Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser	Ser	Ile	Lys	Ile	Ala	Ile	Tyr	Cys
	50					55					60				
Gly	Ile	Val	Ala	Thr	Thr	Pro	Phe	Gly	Val	Tyr	Gln	Val	Ile	Leu	Tyr
65					70					75				80	
Ile	Leu	Pro	Gly	Leu	Thr	Asn	Lys	Glu	Arg	Lys	Val	Ile	Leu	Pro	Ile
				85					90					95	
Leu	Ile	Gly	Ser	Ile	Val	Leu	Phe	Ile	Val	Gly	Gly	Ile	Phe	Ala	Tyr
		100						105					110		
Phe	Val	Leu	Ala	Pro	Ala	Ala	Leu	Asn	Phe	Leu	Ile	Ser	Tyr	Gly	Ala
		115					120					125			
Asp	Ile	Val	Glu	Pro	Leu	Trp	Ser	Phe	Glu	Gln	Tyr	Phe	Asp	Phe	Ile
	130					135					140				
Leu	Leu	Leu	Leu	Phe	Ser	Thr	Gly	Leu	Ala	Phe	Glu	Ile	Pro		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys	Thr	Ile	Leu	Glu	Val	Arg	Ile	Arg	Val	Phe	Trp	Ile	Leu	Ile	
1			5					10					15		
Cys	Phe	Ser	Phe	Thr	Trp	Phe	Thr	Cys	Tyr	Trp	Phe	Ser	Glu	Glu	Phe
			20					25					30		
Ile	Phe	Leu	Leu	Ala	Lys	Pro	Phe	Leu	Thr	Leu	Pro	Tyr	Leu	Asp	Ser
		35					40					45			
Ser	Phe	Ile	Cys	Thr	Gln	Leu	Thr	Glu	Ala	Leu	Ser	Thr	Tyr	Val	Thr
	50					55					60				
Thr	Ser	Leu	Ile	Ser	Cys	Phe	Tyr	Phe	Leu	Phe	Pro	Phe	Leu	Ser	Tyr
65					70					75					80
Gln	Ile	Trp	Cys	Phe	Leu	Met	Pro	Ser	Cys	Tyr	Glu	Glu	Gln	Arg	Lys
				85					90					95	
Lys	Tyr	Asn	Lys	Leu	Phe	Tyr	Leu	Ser	Gly	Phe	Cys	Phe	Phe	Leu	Phe
			100					105					110		
Phe	Phe	Val	Thr	Phe	Val	Trp	Ile	Val	Pro	Asn	Val	Trp	His	Phe	Leu
		115					120					125			
Tyr	Lys	Leu	Ser	Thr	Thr	Ser	Thr	Asn	Leu	Leu	Ile	Ile	Lys	Leu	Gln
	130					135					140				
Pro	Lys	Ile	Phe	Asp	Tyr	Ile	Met	Leu	Thr	Val	Arg	Ile	Leu	Phe	Ile
145					150					155					160
Ser	Ser	Ile	Cys	Ser	Gln	Val	Pro								
					165										

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu	Thr	Ile	Leu	Gly	Glu	Val	Arg	Ile	Arg	Ser	Val	Arg	Ile	Leu	Ile
1			5						10					15	
Gly	Leu	Gly	Leu	Thr	Trp	Phe	Thr	Cys	Tyr	Trp	Phe	Pro	Glu	Glu	Leu
			20					25					30		
Ile	Ser	Pro	Leu	Ala	Ser	Pro	Phe	Leu	Thr	Leu	Pro	Phe	Asp	Ser	Tyr
		35					40					45			
Phe	Val	Cys	Thr	Gln	Leu	Thr	Glu	Ala	Phe	Ser	Thr	Phe	Val	Ala	Thr
	50					55					60				
Ser	Ser	Ile	Ala	Cys	Ser	Tyr	Phe	Val	Phe	Pro	Leu	Ile	Ser	Tyr	Gln

65					70						75				80
Ile	Trp	Cys	Phe	Leu	Ile	Pro	Ser	Cys	Tyr	Gly	Glu	Gln	Arg	Thr	Lys
				85					90					95	
Tyr	Asn	Arg	Phe	Leu	His	Leu	Ser	Gly	Ser	Arg	Phe	Phe	Leu	Phe	Leu
			100					105					110		
Phe	Leu	Thr	Pro	Pro	Arg	Val	Val	Pro	Asn	Val	Trp	His	Phe	Pro	Tyr
		115					120					125			
Phe	Val	Gly	Ala	Thr	Ser	Thr	Asn	Ser	Leu	Met	Ile	Lys	Leu	Gln	Pro
	130					135					140				
Lys	Ile	Tyr	Asp	His	Ile	Met	Leu	Thr	Val	Arg	Ile	Ser	Phe	Ile	Pro
145					150					155					160
Ser	Val	Cys	Ser	Gln	Val	Pro									
				165											

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu	Thr	His	Leu	Tyr	Glu	Ile	Arg	Leu	Arg	Ile	Ile	Tyr	Leu	Leu	Tyr
1				5					10					15	
Ser	Ile	Phe	Leu	Thr	Cys	Phe	Cys	Ser	Tyr	Gln	Tyr	Lys	Glu	Glu	Ile
			20					25					30		
Phe	Tyr	Leu	Leu	Phe	Ile	Pro	Leu	Ser	Lys	Asn	Phe	Ile	Tyr	Thr	Asp
		35					40					45			
Leu	Ile	Glu	Ala	Phe	Ile	Thr	Tyr	Ile	Lys	Leu	Ser	Ile	Ile	Val	Gly
	50					55					60				
Ile	Tyr	Leu	Ser	Tyr	Pro	Ile	Phe	Leu	Tyr	Gln	Ile	Trp	Ser	Phe	Leu
65					70					75					80
Ile	Pro	Gly	Phe	Phe	Leu	Tyr	Glu	Lys	Lys	Leu	Phe	Arg	Leu	Leu	Cys
			85						90					95	
Leu	Thr	Ser	Ile	Phe	Leu	Tyr	Phe	Leu	Gly	Ser	Cys	Ile	Gly	Tyr	Tyr
			100					105					110		
Leu	Leu	Phe	Pro	Ile	Ala	Phe	Thr	Phe	Phe	Leu	Gly	Phe	Gln	Lys	Leu
		115					120					125			
Gly	Lys	Asp	Gln	Leu	Phe	Thr	Ile	Glu	Leu	Gln	Ala	Lys	Ile	His	Glu
	130					135					140				
Tyr	Leu	Ile	Leu	Asn	Thr	Lys	Leu	Ile	Phe	Ser	Leu	Ser	Ile	Cys	Phe
145					150					155					160

Gln Leu Pro

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Phe	Asp	His	Leu	Asp	Glu	Leu	Arg	Thr	Arg	Ile	Phe	Leu	Ser	Leu	Gly
1				5					10					15	
Ala	Val	Leu	Val	Gly	Val	Val	Ala	Cys	Phe	Ile	Phe	Val	Lys	Pro	Leu
			20					25					30		
Val	Gln	Trp	Leu	Gln	Val	Pro	Ala	Gly	Thr	Val	Lys	Phe	Leu	Gln	Leu
		35					40					45			
Ser	Pro	Gly	Glu	Phe	Phe	Phe	Val	Ser	Val	Lys	Val	Ala	Gly	Tyr	Ser
	50					55					60				
Gly	Ile	Leu	Val	Met	Ser	Pro	Phe	Ile	Leu	Tyr	Gln	Ile	Ile	Gln	Phe
65					70					75					80
Val	Leu	Pro	Gly	Leu	Thr	Arg	Arg	Glu	Arg	Arg	Leu	Leu	Gly	Pro	Val
				85					90					95	
Val	Leu	Gly	Ser	Ser	Val	Leu	Phe	Phe	Ala	Gly	Leu	Gly	Phe	Ala	Tyr
			100					105					110		
Tyr	Ala	Leu	Ile	Pro	Ala	Ala	Leu	Lys	Phe	Phe	Val	Ser	Tyr	Gly	Ala
		115					120					125			
Asp	Val	Val	Glu	Gln	Leu	Trp	Ser	Ile	Asp	Lys	Tyr	Phe	Glu	Phe	Val
	130					135					140				
Leu	Leu	Leu	Met	Phe	Ser	Thr	Gly	Leu	Ala	Phe	Gln	Ile	Pro		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Val	Asp	His	Leu	Thr	Glu	Leu	Arg	Thr	Arg	Leu	Leu	Ile	Ser	Leu	Ala
1				5					10					15	
Ala	Ile	Leu	Val	Thr	Thr	Ile	Phe	Gly	Phe	Val	Trp	Tyr	Ser	His	Ser
			20					25					30		

Ile Phe Gly Leu Asp Ser Leu Gly Glu Trp Leu Arg His Pro Tyr Cys
 35 40 45
 Ala Leu Pro Gln Ser Ala Arg Ala Asp Ile Ser Ala Asp Gly Glu Cys
 50 55 60
 Arg Leu Leu Ala Thr Ala Pro Phe Asp Gln Phe Met Leu Arg Leu Lys
 65 70 75 80
 Val Gly Met Ala Ala Gly Ile Val Leu Ala Cys Pro Val Trp Phe Tyr
 85 90 95
 Gln Leu Trp Ala Phe Ile Thr Pro Gly Leu Tyr Gln Arg Glu Arg Arg
 100 105 110
 Phe Ala Val Ala Phe Val Ile Pro Ala Ala Val Leu Phe Val Ala Gly
 115 120 125
 Ala Val Leu Ala Tyr Leu Val Leu Ser Lys Ala Leu Gly Phe Leu Leu
 130 135 140
 Thr Val Gly Ser Asp Val Gln Val Thr Ala Leu Ser Gly Asp Arg Tyr
 145 150 155 160
 Phe Gly Phe Leu Leu Asn Leu Leu Val Val Phe Gly Val Ser Phe Glu
 165 170 175
 Phe Pro

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

His Leu Gln Glu Leu Arg Lys Arg Leu Met Val Ser Val Gly Thr Ile
 1 5 10 15
 Leu Val Ala Phe Leu Gly Cys Phe His Phe Trp Lys Ser Ile Phe Glu
 20 25 30
 Phe Val Lys Asn Ser Tyr Lys Gly Thr Leu Ile Gln Leu Ser Pro Ile
 35 40 45
 Glu Gly Val Met Val Ala Val Lys Ile Ser Phe Ser Ala Ala Ile Val
 50 55 60
 Ile Ser Met Pro Ile Ile Phe Trp Gln Leu Trp Leu Phe Ile Ala Pro
 65 70 75 80
 Gly Leu Tyr Lys Asn Glu Lys Lys Val Ile Leu Pro Phe Val Phe Phe
 85 90 95
 Gly Ser Gly Met Phe Leu Ile Gly Ala Ala Phe Ser Tyr Tyr Val Val
 100 105 110

Phe	Pro	Phe	Ile	Ile	Glu	Tyr	Leu	Ala	Thr	Phe	Gly	Ser	Asp	Val	Phe
		115					120					125			
Ala	Ala	Asn	Ile	Ser	Ala	Ser	Ser	Tyr	Val	Ser	Phe	Phe	Thr	Arg	Leu
	130					135					140				
Ile	Leu	Gly	Phe	Gly	Val	Ala	Phe	Glu	Leu	Pro					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Thr	His	Leu	Val	Glu	Leu	Arg	Asn	Arg	Leu	Leu	Arg	Cys	Val	Ile
1				5					10					15	
Cys	Val	Val	Leu	Val	Phe	Val	Ala	Leu	Val	Tyr	Phe	Ser	Asn	Asp	Ile
			20					25					30		
Tyr	His	Phe	Val	Ala	Ala	Pro	Leu	Thr	Ala	Val	Met	Pro	Lys	Gly	Ala
		35					40					45			
Thr	Met	Ile	Ala	Thr	Asn	Ile	Gln	Thr	Pro	Phe	Phe	Thr	Pro	Ile	Lys
	50					55					60				
Leu	Thr	Ala	Ile	Val	Ala	Ile	Phe	Ile	Ser	Val	Pro	Tyr	Leu	Leu	Tyr
65					70					75					80
Gln	Ile	Trp	Ala	Phe	Ile	Ala	Pro	Ala	Leu	Tyr	Gln	His	Glu	Lys	Arg
				85					90					95	
Met	Ile	Tyr	Pro	Leu	Leu	Phe	Ser	Ser	Thr	Ile	Leu	Phe	Tyr	Cys	Gly
			100					105					110		
Val	Ala	Phe	Ala	Tyr	Tyr	Ile	Val	Phe	Pro	Leu	Val	Phe	Ser	Phe	Phe
		115					120					125			
Thr	Gln	Thr	Ala	Pro	Glu	Gly	Val	Thr	Ile	Ala	Thr	Asp	Ile	Ser	Ser
	130					135					140				
Tyr	Leu	Asp	Phe	Ala	Leu	Ala	Leu	Phe	Leu	Ala	Phe	Gly	Val	Cys	Phe
145					150					155					160
Glu	Val	Pro													

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Leu Glu His Ile Ala Glu Leu Arg Lys Arg Leu Leu Ile Val Ala Leu
1           5           10           15
Ala Phe Val Val Phe Phe Ile Ala Gly Phe Phe Leu Ala Lys Pro Ile
20           25           30
Ile Val Tyr Leu Gln Glu Thr Asp Glu Ala Lys Gln Leu Thr Leu Asn
35           40           45
Ala Phe Asn Leu Thr Asp Pro Leu Tyr Val Phe Met Gln Phe Ala Phe
50           55           60
Ile Ile Gly Ile Val Leu Thr Ser Pro Val Ile Leu Tyr Gln Leu Trp
65           70           75           80
Ala Phe Val Ser Pro Gly Leu Tyr Glu Lys Glu Arg Lys Val Thr Leu
85           90           95
Ser Tyr Ile Pro Val Ser Ile Leu Leu Phe Leu Ala Gly Leu Ser Phe
100          105          110
Ser Tyr Tyr Ile Leu Phe Pro Phe Val Val Asp Phe Met Lys Arg Ile
115          120          125
Ser Gln Asp Leu Asn Val Asn Gln Val Ile Gly Ile Asn Glu Tyr Phe
130          135          140
His Phe Leu Leu Gln Leu Thr Ile Pro Phe Gly Leu Leu Phe Gln Met
145          150          155          160
Pro
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Val Ala His Leu Thr Glu Leu Arg Ser Arg Leu Leu Arg Ser Val Ala
1           5           10           15
Ala Val Leu Leu Ile Phe Ala Ala Leu Phe Tyr Phe Ala Gln Asp Ile
20           25           30
Tyr Ala Leu Val Ser Ala Pro Leu Arg Ala Tyr Leu Pro Glu Gly Ala
35           40           45
Thr Met Ile Ala Thr Gly Val Ala Ser Pro Phe Leu Ala Pro Phe Lys
50           55           60
Leu Thr Leu Met Ile Ser Leu Phe Leu Ala Met Pro Val Val Leu His
```

65		70		75		80									
Gln	Val	Trp	Gly	Phe	Ile	Ala	Pro	Gly	Leu	Tyr	Gln	His	Glu	Lys	Arg
			85						90					95	
Ile	Ala	Met	Pro	Leu	Met	Ala	Ser	Ser	Val	Leu	Leu	Phe	Tyr	Ala	Gly
			100					105					110		
Met	Ala	Phe	Ala	Tyr	Phe	Val	Val	Phe	Pro	Ile	Met	Phe	Gly	Phe	Phe
		115					120					125			
Ala	Ser	Val	Thr	Pro	Glu	Gly	Val	Ala	Met	Met	Thr	Asp	Ile	Gly	Gln
		130				135					140				
Tyr	Leu	Asp	Phe	Val	Leu	Thr	Leu	Phe	Phe	Ala	Phe	Gly	Val	Ala	Phe
145					150					155					160
Glu	Val	Pro													

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ile	Ala	Leu	Ile	Val	Ile	Val	Val	Ser	Ser	Leu	Phe	Phe	Thr	Phe	Gly
1			5					10						15	
Ala	Asn	Ile	Val	Val	Gly	Lys	Ile	Ile	Gly	Asp	Leu	Phe	Pro	Gly	Glu
		20					25						30		
Ala	Val	Ile	Glu	Asn	Arg	Asp	Lys	Ile	Leu	Ala	Ile	Ala	Glu	Glu	Leu
		35					40					45			
Lys	Lys	Ile	Ala	Ser	Asp	Leu	Glu	Asn	Tyr	Ala	Tyr	His	Pro	Ser	Glu
	50					55					60				
Ala	Asn	Arg	Ser	Ile	Ala	Phe	Ala	Ala	Ser	Lys	Ser	Leu	Val	Arg	Ile
65				70					75					80	
Ala	Met	Gln	Leu	Ser	Thr	Ser	Pro	Val	Leu	Leu	Thr	Pro	Leu	Glu	Gly
			85					90						95	
Leu	Leu	Leu	Tyr	Leu	Lys	Ile	Ser	Leu	Ala	Val	Gly	Ile	Ala	Ala	Ala
		100					105					110			
Leu	Pro	Tyr	Ile	Phe	His	Leu	Val	Leu	Thr	Ala	Leu	Arg	Glu	Arg	Gly
		115				120						125			
Val	Ile	Thr	Phe	Ser	Phe	Arg	Lys	Thr	Ser	Ala	Phe	Lys	Tyr	Gly	Met
	130					135					140				
Ala	Ala	Ile	Phe	Leu	Phe	Ala	Leu	Gly	Ile	Phe	Tyr	Gly	Tyr	Asn	Met
145				150						155					160

Met Lys Phe Phe Ile Lys Phe Leu Tyr Leu Met Ala Val Ser Gln Gly
165 170 175
Ala Ile Pro Leu Tyr Ser Leu Ser Glu Phe Val Asn Phe Val Ala Leu
180 185 190
Met Leu Val Leu Phe Gly Ile Val Phe Glu Leu Pro
195 200

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Val Glu Asp Leu Arg Arg Leu Ala Ala Glu Glu Gly Val Val Ala
1 5 10 15
Leu Gly Glu Thr Gly Leu Asp Tyr Tyr Tyr Thr Pro Glu Thr Lys Val
20 25 30
Arg Gln Gln Glu Ser Phe Ile His His Ile Gln Ile Gly Arg Glu Leu
35 40 45
Asn Lys Pro Val Ile Val His Thr Arg Asp Ala Arg Ala Asp Thr Leu
50 55 60
Ala Ile Leu Arg Glu Glu Lys Val Thr Asp Cys Gly Gly Val Leu His
65 70 75 80
Cys Phe Thr Glu Asp Arg Glu Thr Ala Gly Lys Leu Leu Asp Leu Gly
85 90 95
Phe Tyr Ile Ser Phe Ser Gly Ile Val Thr Phe Arg Asn Ala Glu Gln
100 105 110
Leu Arg Asp Ala Ala Arg Tyr Val Pro Leu Asp Arg Leu Leu Val Glu
115 120 125
Thr Asp Ser Pro Tyr Leu Ala Pro
130 135

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Leu Glu Gln Leu Gln Gln Ala Leu Glu Arg Arg Pro Ala Lys Val
1 5 10 15

Val Ala Val Gly Glu Ile Gly Leu Asp Leu Phe Gly Asp Asp Pro Gln
 20 25 30
 Phe Glu Arg Gln Gln Trp Leu Leu Asp Glu Gln Leu Lys Leu Ala Lys
 35 40 45
 Arg Tyr Asp Leu Pro Val Ile Leu His Ser Arg Arg Thr His Asp Lys
 50 55 60
 Leu Ala Met His Leu Lys Arg His Asp Leu Pro Arg Thr Gly Val Val
 65 70 75 80
 His Gly Phe Ser Gly Ser Leu Gln Gln Ala Glu Arg Phe Val Gln Leu
 85 90 95
 Gly Tyr Lys Ile Gly Val Gly Gly Thr Ile Thr Tyr Pro Arg Ala Ser
 100 105 110
 Lys Thr Arg Asp Val Ile Ala Lys Leu Pro Leu Ala Ser Leu Leu Leu
 115 120 125
 Glu Thr Asp Ala Pro Asp Met Pro Leu
 130 135

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Ile Gly Glu Val Val Ser Gln Ile Glu Ser Asn Ile Asp Leu Ile
 1 5 10 15
 Val Ala Val Gly Glu Thr Gly Met Asp Phe His His Thr Arg Asp Glu
 20 25 30
 Glu Gly Arg Arg Arg Gln Glu Glu Thr Phe Arg Val Phe Val Glu Leu
 35 40 45
 Ala Ala Glu His Glu Met Pro Leu Val Val His Ala Arg Asp Ala Glu
 50 55 60
 Glu Arg Ala Leu Glu Thr Val Leu Glu Tyr Arg Val Pro Glu Val Ile
 65 70 75 80
 Phe His Cys Tyr Gly Gly Ser Ile Glu Thr Ala Arg Arg Ile Leu Asp
 85 90 95
 Glu Gly Tyr Tyr Ile Ser Ile Ser Thr Leu Val Ala Phe Ser Glu His
 100 105 110
 His Met Glu Leu Val Arg Ala Ile Pro Leu Glu Gly Met Leu Thr Glu
 115 120 125
 Thr Asp Ser Pro Tyr Leu Ser
 130 135

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Ala Gln Ala Thr Leu Lys Lys Leu Val Ser Thr His Arg Ser Phe Ile
 1              5              10              15

Ser Cys Ile Gly Glu Tyr Gly Phe Asp Tyr His Tyr Thr Lys Asp Tyr
          20              25              30

Ile Thr Gln Gln Glu Gln Phe Phe Leu Met Gln Phe Gln Leu Ala Glu
      35              40              45

Gln Tyr Gln Leu Val His Met Leu His Val Arg Asp Val His Glu Arg
 50              55              60

Ile Tyr Glu Val Leu Lys Arg Leu Lys Pro Lys Gln Pro Val Val Phe
 65              70              75              80

His Cys Phe Ser Glu Asp Thr Asn Thr Ala Leu Lys Leu Leu Thr Leu
          85              90              95

Arg Glu Val Gly Leu Lys Val Tyr Phe Ser Ile Pro Gly Ile Val Thr
      100              105              110

Phe Lys Asn Ala Lys Asn Leu Gln Ala Ala Leu Ser Val Ile Pro Thr
      115              120              125

Glu Leu Leu Leu Ser Glu Thr Asp Ser Pro Tyr Leu Ala Pro
      130              135              140
```

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Ala Arg Ala Glu Leu Glu Arg Leu Val Ala His Pro Arg Val Val Ala
 1              5              10              15

Val Gly Glu Thr Gly Ile Asp Met Tyr Trp Pro Gly Arg Leu Asp Gly
      20              25              30

Cys Ala Glu Pro His Val Gln Arg Glu Ala Phe Ala Trp His Ile Asp
      35              40              45

Leu Ala Lys Arg Thr Gly Lys Pro Leu Met Ile His Asn Arg Gln Ala
      50              55              60
```

Asp	Arg	Asp	Val	Leu	Asp	Val	Leu	Arg	Ala	Glu	Gly	Ala	Pro	Asp	Thr
65					70					75					80
Val	Ile	Leu	His	Cys	Phe	Ser	Ser	Asp	Ala	Ala	Met	Ala	Arg	Thr	Cys
				85					90					95	
Val	Asp	Ala	Gly	Trp	Leu	Leu	Ser	Leu	Ser	Gly	Thr	Val	Ser	Phe	Arg
			100					105					110		
Thr	Ala	Arg	Glu	Leu	Arg	Glu	Ala	Val	Pro	Leu	Met	Pro	Val	Glu	Gln
		115					120					125			
Leu	Leu	Val	Glu	Thr	Asp	Ala	Pro	Tyr	Leu	Thr	Pro				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp	Glu	Ser	Leu	Phe	Glu	Lys	Phe	Val	Gly	His	Gln	Lys	Cys	Val	Ala
1				5					10					15	
Ile	Gly	Glu	Cys	Gly	Leu	Asp	Tyr	Tyr	Arg	Leu	Pro	Glu	Leu	Asn	Glu
			20					25					30		
Arg	Glu	Asn	Tyr	Lys	Ser	Lys	Gln	Lys	Glu	Ile	Phe	Thr	Lys	Gln	Ile
		35					40					45			
Glu	Phe	Ser	Ile	Gln	His	Asn	Lys	Pro	Leu	Ile	Ile	His	Ile	Arg	Glu
	50					55					60				
Ala	Ser	Phe	Asp	Ser	Leu	Asn	Leu	Leu	Lys	Asn	Tyr	Pro	Lys	Ala	Phe
65					70					75					80
Gly	Val	Leu	His	Cys	Phe	Asn	Ala	Asp	Gly	Met	Leu	Leu	Glu	Leu	Ser
				85					90				95		
Asp	Arg	Phe	Tyr	Tyr	Gly	Ile	Gly	Gly	Val	Ser	Thr	Phe	Lys	Asn	Ala
			100				105						110		
Lys	Arg	Leu	Val	Glu	Ile	Leu	Pro	Lys	Ile	Pro	Lys	Asn	Arg	Leu	Leu
		115					120					125			
Leu	Glu	Thr	Asp	Ser	Pro	Tyr	Leu	Thr	Pro						
	130					135									

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Asp Ala Glu Arg Leu Leu Arg Leu Ala Gln Asp Pro Lys Val Ile Ala
1      5      10      15
Ile Gly Glu Ile Gly Leu Asp Tyr Tyr Tyr Ser Ala Asp Asn Lys Ala
20     25     30
Ala Gln Gln Ala Val Phe Gly Ser Gln Ile Asp Ile Ala Asn Gln Leu
35     40     45
Asp Lys Pro Val Ile Ile His Thr Arg Ser Ala Gly Asp Asp Thr Ile
50     55     60
Ala Met Leu Arg Gln His Arg Ala Glu Lys Cys Gly Gly Val Ile His
65     70     75     80
Cys Phe Thr Glu Thr Met Glu Phe Xaa Lys Lys Ala Leu Asp Leu Gly
85     90     95
Phe Tyr Ile Ser Cys Ser Gly Ile Val Thr Phe Lys Asn Ala Glu Ala
100    105    110
Ile Arg Glu Val Ile Arg Tyr Val Pro Met Glu Arg Leu Leu Val Glu
115    120    125
Thr Asp Ser Pro Tyr Leu Ala Pro
130    135
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Asp Leu Ala Trp Ile Lys Glu Leu Ser Ala His Glu Lys Val Val Ala
1      5      10      15
Ile Gly Glu Met Gly Leu Asp Tyr His Trp Asp Lys Ser Pro Lys Asp
20     25     30
Ile Gln Lys Glu Val Phe Arg Asn Gln Ile Ala Leu Ala Lys Glu Val
35     40     45
Asn Leu Pro Ile Ile Ile His Asn Arg Asp Ala Thr Glu Asp Val Val
50     55     60
Thr Ile Leu Lys Glu Glu Gly Ala Glu Ala Val Gly Gly Ile Met His
65     70     75     80
Cys Phe Thr Gly Ser Ala Glu Val Ala Arg Glu Cys Met Lys Met Asn
85     90     95
Phe Tyr Leu Ser Phe Gly Gly Pro Val Thr Phe Lys Asn Ala Lys Lys
```

100	105	110
Pro Lys Glu Val Val Lys Glu Ile	Pro Asn Asp Arg Leu	Leu Ile Glu
115	120	125
Thr Asp Cys Pro Phe Leu Thr Pro		
130	135	

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Glu	Ala	Leu	Ala	Asn	Lys	Gly	Lys	Ala	Ser	Gly	Lys	Val	Val	Ala	Phe
1				5					10					15	
Gly	Glu	Phe	Gly	Leu	Asp	Tyr	Asp	Arg	Leu	His	Tyr	Ala	Pro	Ala	Asp
			20					25					30		
Val	Gln	Lys	Met	Tyr	Phe	Glu	Glu	Gln	Leu	Lys	Val	Ala	Val	Arg	Val
		35					40					45			
Gln	Leu	Pro	Leu	Phe	Leu	His	Ser	Arg	Asn	Ala	Glu	Asn	Asp	Phe	Phe
	50					55					60				
Ala	Ile	Leu	Glu	Lys	Tyr	Leu	Pro	Glu	Leu	Pro	Lys	Lys	Gly	Val	Val
65				70						75				80	
His	Ser	Phe	Thr	Gly	Ser	Ile	Asp	Glu	Met	Arg	Arg	Cys	Ile	Glu	His
				85					90					95	
Gly	Leu	Tyr	Val	Gly	Val	Asn	Gly	Cys	Ser	Leu	Lys	Thr	Glu	Glu	Asn
			100					105					110		
Leu	Glu	Val	Val	Arg	Ala	Ile	Pro	Leu	Glu	Lys	Met	Leu	Leu	Glu	Thr
		115					120					125			
Asp	Ala	Pro	Trp	Cys	Glu	Val									
		130				135									

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

His	Ile	Ser	Lys	Met	Glu	Gln	Phe	Phe	Val	Glu	His	Glu	Arg	Asp	Ile
1				5					10					15	

Ile Cys Val Gly Glu Cys Gly Leu Asp His Thr Ile Ser Gln Phe Lys
 20 25 30
 Leu Thr Thr Glu Asp Phe Glu Glu Gln Glu Thr Val Phe Lys Trp Gln
 35 40 45
 Ile Asp Leu Ala Lys His Phe Glu Lys Pro Leu Ile Leu Glu Ile Pro
 50 55 60
 Asp Ile Ser Arg Asn Val His Ser Arg Ser Ala Ala Arg Arg Thr Ile
 65 70 75 80
 Glu Ile Leu Leu Glu Cys His Val Ala Pro Asp Gln Val Val Leu His
 85 90 95
 Ala Phe Asp Gly Thr Pro Gly Asp Leu Lys Leu Gly Leu Glu Ala Gly
 100 105 110
 Tyr Leu Phe Ser Ile Pro Pro Ser Phe Gly Lys Ser Glu Glu Thr Thr
 115 120 125
 Gln Leu Ile Glu Ser Ile Pro Leu Ser Gln Leu Leu Leu Glu Thr Asp
 130 135 140
 Ser Pro Ala Leu Gly
 145

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Glu Arg Asn Leu Leu Gln Ala Leu Arg His Pro Lys Ala Val Ala
 1 5 10 15
 Phe Gly Glu Met Gly Leu Asp Tyr Ser Tyr Lys Cys Thr Thr Pro Val
 20 25 30
 Pro Glu Gln His Lys Val Phe Glu Arg Gln Leu Gln Leu Ala Val Ser
 35 40 45
 Leu Lys Lys Pro Leu Val Ile His Cys Arg Glu Ala Asp Glu Asp Leu
 50 55 60
 Leu Glu Ile Met Lys Lys Phe Val Pro Pro Asp Tyr Lys Ile His Arg
 65 70 75 80
 His Cys Phe Thr Gly Ser Tyr Pro Val Ile Glu Pro Leu Leu Lys Tyr
 85 90 95
 Phe Pro Asn Met Ser Val Gly Phe Thr Ala Val Leu Thr Tyr Ser Ser
 100 105 110
 Ala Trp Glu Ala Arg Glu Ala Leu Arg Gln Ile Pro Leu Glu Arg Ile
 115 120 125

Ile Val Glu Thr Asp Ala Pro Tyr Phe Leu Pro
130 135

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Arg Arg Ser Phe Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Arg Arg Ser Phe Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Lys Thr Lys Ile Pro Asp Ala Val Leu Ala Ala Glu Val Ser Arg
1 5 10 15

Arg Gly Leu Val Lys Thr Thr Ile Ala Phe Phe Leu Ala Met Ala Ser
20 25 30

Ser Ala Leu Thr Leu Pro Phe Ser Arg Ile Ala His Ala Val Asp Ser
35 40 45

Ala Ile
50

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid


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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
TTAGTCGGAT TAATCACAAT GTCGATAGCG                                     30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
ATTCTGGCTG GGTGCCACCA GATACCAACG TTGAAGAGTT CGAATTTGCC ATTCGTACGG      60
TCTGTGAACC TATCTTTGAG AAACCGCTGG CCGAAATTTT GTTTGGACAT GTACTGTAA      120
ATCTGTTTAA TACGGCGCGT CGCTTCAATA TGGAAGTGCA GCCGCAACTG GTGTTACTCC      180
AGAAAACCCT GCTCTACGTC GAAGGGGTAG GACGCCAGCT TTATCCGCAA CTCGATTTAT      240
GGAAAACGGC GAAGCCTTTC CTGGAGTCGT GGATTAAAGA TCAGGTCGGT ATTCCTGCGC      300
TGGTGAGAGC ATTTAAAGAA AAAGCGCCGT TCTGGGTCGA AAAAATGCCA GAACTGCCTG      360
AATTGGTTTA CGACAGTTTG CGCCAGGGCA AGTATTTACA GCACAGTGTT GATAAGATTG      420
CCCGCGAGCT TCAGTCAAAT CATGTACGTC AGGGACAATC GCGTTATTTT CTCGGAATTG      480
GCGCTACGTT AGTATTAAGT GGCACATTCT TGTTGGTCAG CCGACCTGAA TGGGGGCTGA      540
TGCCCGGCTG GTTAATGGCA GGTGGTCTGA TCGCCTGGTT TGTCGGTTGG CGCAAAACAC      600
GCTGATTTTT TCATCGCTCA AGGCGGGCCG TGTAACGTAT AATGCGGCTT TGTTTAATCA      660
TCATCTACCA CAGAGGAACA TGTATGGGTG GTATCAGTAT TTGGCAGTTA TTGATTATTG      720
CCGTCATCGT TGTACTGCTT TTTGGCACCA AAAAGCTCGG CTCCATCGGT TCCGATCTTG      780
GTGCGTCGAT CAAAGGCTTT AAAAAAGCAA TGAGCGATGA TGAACCAAAG CAGGATAAAA      840
CCAGTCAGGA TGCTGATTTT ACTGCGAAAA CTATCGCCGA TAAGCAGGCG GATACGAATC      900
AGGAACAGGC TAAACAGAA GACGCGAAGC GCCACGATAA AGAGCAGGTG TAATCCGTGT      960
TTGATATCGG TTTTAGCGAA CTGCTATTGG TGTTTCATCAT CGGCCTCGTC GTTCTGGGGC     1020
CGCAACGACT GCCTGTGGCG GTAAAAACGG TAGCGGGCTG GATTCGCGCG TTGCGTTCAC     1080
TGGCGACAAC GGTGCAGAAC GAACTGACCC AGGAGTTAAA ACTCCAGGAG TTTCAGGACA     1140
GTCTGAAAAA GGTTGAAAAG GCGAGCCTCA CTAACCTGAC GCCCGAACTG AAAGCGTCGA     1200

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TGGATGAACT	ACGCCAGGCC	GCGGAGTCGA	TGAAGCGTTC	CTACGTTGCA	AACGATCCTG	1260
AAAAGGCGAG	CGATGAAAGCG	CACACCATCC	ATAACCCGGT	GGTGAAAGAT	AATGAAGCTG	1320
CGCATGAGGG	CGTAACGCCT	GCCGCTGCAC	AAACGCAGGC	CAGTTCGCCG	GAACAGAAGC	1380
CAGAAACCAC	GCCAGAGCCG	GTGGTAAAAC	CTGCTGCGGA	CGCTGAACCG	AAAACCGCTG	1440
CACCTTCCCC	TTCGTCGAGT	GATAAACCGT	AAACATGTCT	GTAGAAGATA	CTCAACCGCT	1500
TATCACGCAT	CTGATTGAGC	TGCGTAAGCG	TCTGCTGAAC	TGCATTATCG	CGGTGATCGT	1560
GATATTCCCTG	TGTCTGGTCT	ATTTTCGCCAA	TGACATCTAT	CACCTGGTAT	CCGCGCCATT	1620
GATCAAGCAG	TTGCCGCAAG	GTTCAACGAT	GATCGCCACC	GACGTGGCCT	CGCCGTTCTT	1680
TACGCCGATC	AAGCTGACCT	TTATGGTGTC	GCTGATTCTG	TCAGCGCCGG	TGATTCTCTA	1740
TCAGGTGTGG	GCATTTATCG	CCCCAGCGCT	GTATAAGCAT	GAACGTCGCC	TGGTGGTGCC	1800
GCTGCTGGTT	TCCAGCTCTC	TGCTGTTTTA	TATCGGCATG	GCATTCGCCT	ACTTTGTGGT	1860
CTTTCCGCTG	GCATTTGGCT	TCCTTGCCAA	TACCGCGCCG	GAAGGGGTGC	AGGTATCCAC	1920
CGACATCGCC	AGCTATTTAA	GCTTCGTTAT	GGCGCTGTTT	ATGGCGTTTG	GTGTCTCCTT	1980
TGAAGTGCCG	GTAGCAATTG	TGCTGCTGTG	CTGGATGGGG	ATTACCTCGC	CAGAAGACTT	2040
ACGCAAAAAA	CGCCCGTATG	TGCTGGTTGG	TGCATTCTGT	GTCGGGATGT	TGCTGACGCC	2100
GCCGGATGTC	TTCTCGCAAA	CGCTGTTGGC	GATCCCGATG	TACTGTCTGT	TTGAAATCGG	2160
TGTCTTCTTC	TCACGCTTTT	ACGTTGGTAA	AGGGCGAAAT	CGGGAAGAGG	AAAACGACGC	2220
TGAAGCAGAA	AGCGAAAAAA	CTGAAGAATA	AATTCAACCG	CCCGTCAGGG	CGGTTGTCAT	2280
ATGGAGTACA	GGATGTTTGA	TATCGGCGTT	AATTTGACCA	GTTTCGCAAT	TGCGAAAGAC	2340
CGTGATGATG	TTGTAGCGTG	CGCTTTTGAC	GCGGGAGTTA	ATGGGCTACT	CATCACCGGC	2400
ACTAACCTGC	GTGAAAGCCA	GCAGGCGCAA	AAGCTGGCGC	GTCAGTATTC	GTCCTGTTGG	2460
TCAACGGCGG	GCGTACATCC	TCACGACAGC	AGCCAGTGCG	AAGCTGCGAC	TGAAGAAGCG	2520
ATTATTGAGC	TGGCCGCGCA	GCCAGAAGTG	GTGGCGATTG	GTGAATGTGG	TCTCGACTTT	2580
AACCGCAACT	TTTCGACGCC	GGAAGAGCAG	GAACGCGCTT	TTGTTGCCCA	GCTACGCATT	2640
GCCGCAGATT	TAAACATGCC	GGTATTTATG	CACTGTCGCG	ATGCCACAGA	GCGGTTTATG	2700
ACATTGCTGG	AGCCGTGGCT	GGATAAACTG	CCTGGTGCGG	TTCTTCATTG	CTTTACCGGC	2760
ACACGCGAAG	AGATGCAGGC	GTGCGTGGCG	CATGGAATTT	ATATCGGCAT	TACCGGTTGG	2820
GTTTGCGATG	AACGACGCGG	ACTGGAGCTG	CGGGAACTTT	TGCCGTTGAT	TCCGGCGGAA	2880
AAATTACTGA	TCGAAACTGA	TGCGCCGTAT	CTGCTCCCTC	GCGATCTCAC	GCCAAAGCCA	2940
TCATCCCGGC	GCAACGAGCC	AGCCCATCTG	CCCCATATTT	TGCAACGTAT	TGCGCACTGG	3000
CGTGGAGAAG	ATGCCGCATG	GCTGGCTGCC	ACCACGGATG	CTAATGCCAA	AACACTGTTT	3060

GGGATTGCGT TTTAGAGTTT GCGGAAC TCG GTATTCTTCA CACTGTGCTT AATCTCTTTA 3120

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGCGGCTTT GTTTAATCAT CATCTACCAC AGAGGAACAT GTATGGGTGG TATCAGTATT	60
TGGCAGTTAT TGATTATTGC CGTCATCGTT GTACTGCTTT TTGGCACCAA AAAGCTCGGC	120
TCCATCGGTT CCGATCTTGG TCGTCGATC AAAGGCTTTA AAAAAGCAAT GAGCGATGAT	180
GAACCAAAGC AGGATAAAAC CAGTCAGGAT GCTGATTTTA CTGCGAAAAC TATCGCCGAT	240
AAGCAGGCGG ATACGAATCA GGAACAGGCT AAAACAGAAG ACGCGAAGCG CCACGATAAA	300
GAGCAGGTGT AA	312

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Arg Leu Cys Leu Ile Ile Ile Tyr His Arg Gly Thr Cys Met Gly	
1 5 10 15	
Gly Ile Ser Ile Trp Gln Leu Leu Ile Ile Ala Val Ile Val Val Leu	
20 25 30	
Leu Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu Gly Ala	
35 40 45	
Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro Lys Gln	
50 55 60	
Asp Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile Ala Asp	
65 70 75 80	
Lys Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Thr Glu Asp Ala Lys	
85 90 95	
Arg His Asp Lys Glu Gln Val	
100	

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TGTTTGATAT CGGTTTTAGC GAACTGCTAT TGGTGTTTCAT CATCGGCCTC GTCGTTCTGG	60
GGCCGCAACG ACTGCCTGTG GCGGTAAAAA CGGTAGCGGG CTGGATTTCGC GCGTTGCGTT	120
CACTGGCGAC AACGGTGCAG AACGAACTGA CCCAGGAGTT AAAACTCCAG GAGTTTCAGG	180
ACAGTCTGAA AAAGGTTGAA AAGGCGAGCC TCACTAACCT GACGCCCCGAA CTGAAAGCGT	240
CGATGGATGA ACTACGCCAG GCCGCGGAGT CGATGAAGCG TTCCTACGTT GCAAACGATC	300
CTGAAAAGGC GAGCGATGAA GCGCACACCA TCCATAACCC GGTGGTGAAA GATAATGAAG	360
CTGCGCATGA GGGCGTAACG CCTGCCGCTG CACAAACGCA GGCCAGTTCG CCGGAACAGA	420
AGCCAGAAAC CACGCCAGAG CCGGTGGTAA AACCTGCTGC GGACGCTGAA CCGAAAACCG	480
CTGCACCTTC CCCTTCGTCG AGTGATAAAC CGTAA	515

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Phe Asp Ile Gly Phe Ser Glu Leu Leu Val Phe Ile Ile Gly	
1 5 10 15	
Leu Val Val Leu Gly Pro Gln Arg Leu Pro Val Ala Val Lys Thr Val	
20 25 30	
Ala Gly Trp Ile Arg Ala Leu Arg Ser Leu Ala Thr Thr Val Gln Asn	
35 40 45	
Glu Leu Thr Gln Glu Leu Lys Leu Gln Glu Phe Gln Asp Ser Leu Lys	
50 55 60	
Lys Val Glu Lys Ala Ser Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala	
65 70 75 80	
Ser Met Asp Glu Leu Arg Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr	
85 90 95	
Val Ala Asn Asp Pro Glu Lys Ala Ser Asp Glu Ala His Thr Ile His	
100 105 110	
Asn Pro Val Val Lys Asp Asn Glu Ala Ala His Glu Gly Val Thr Pro	
115 120 125	

Ala Ala Ala Gln Thr Gln Ala Ser Ser Pro Glu Gln Lys Pro Glu Thr
130 135 140
Thr Pro Glu Pro Val Val Lys Pro Ala Ala Asp Ala Glu Pro Lys Thr
145 150 155 160
Ala

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Glu Ala Arg Met Thr Gly Arg Arg Lys Val Thr Arg Arg Asp Ala
1 5 10 15
Met Ala Asp Ala Ala Arg Ala Val Gly Val Ala Cys Leu Gly Gly Phe
20 25 30
Ser Leu Ala Ala Leu Val Arg Thr Ala Ser Pro Val Asp Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ser Arg Ser Ala Lys Pro Gln Asn Gly Arg Arg Arg Phe Leu Arg
1 5 10 15
Asp Val Val Arg Thr Ala Gly Gly Leu Ala Ala Val Gly Val Ala Leu
20 25 30
Gly Leu Gln Gln Gln Thr Ala Arg Ala
35 40

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Thr Trp Ser Arg Arg Gln Phe Leu Thr Gly Val Gly Val Leu Ala
 1 5 10 15

Ala Val Ser Gly Thr Ala Gly Arg Val Val Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Asp Arg Arg Arg Phe Leu Thr Leu Leu Gly Ser Ala Gly Leu Thr
 1 5 10 15

Ala Thr Val Ala Thr Ala Gly Thr Ala Lys Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ser Glu Lys Asp Lys Met Ile Thr Arg Arg Asp Ala Leu Arg Asn
 1 5 10 15

Ile Ala Val Val Val Gly Ser Val Ala Thr Thr Thr Met Met Gly Val
 20 25 30

Gly Val Ala Asp Ala
 35

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Gln Ile Val Asn Leu Thr Arg Arg Gly Phe Leu Lys Ala Ala Cys
 1 5 10 15

Val Val Thr Gly Gly Ala Leu Ile Ser Ile Arg Met Thr Gly Lys Ala
 20 25 30

Val Ala

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Asn	Asn	Glu	Glu	Thr	Phe	Tyr	Gln	Ala	Met	Arg	Arg	Gln	Gly	Val
1				5					10					15	
Thr	Arg	Arg	Ser	Phe	Leu	Lys	Tyr	Cys	Ser	Leu	Ala	Ala	Thr	Ser	Leu
			20					25					30		
Gly	Leu	Gly	Ala	Gly	Met	Ala	Pro	Lys	Ile	Ala	Trp	Ala			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Ser	Thr	Gly	Thr	Thr	Asn	Leu	Val	Arg	Thr	Leu	Asp	Ser	Met	Asp
1				5					10					15	
Phe	Leu	Lys	Met	Asp	Arg	Arg	Thr	Phe	Met	Lys	Ala	Val	Ser	Ala	Leu
			20					25					30		
Gly	Ala	Thr	Ala	Phe	Leu	Gly	Thr	Tyr	Gln	Thr	Glu	Ile	Val	Asn	Ala
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Lys	Cys	Tyr	Ile	Gly	Arg	Gly	Lys	Asn	Gln	Val	Glu	Glu	Arg	Leu
1				5					10					15	
Glu	Arg	Arg	Gly	Val	Ser	Arg	Arg	Asp	Phe	Met	Lys	Phe	Cys	Thr	Ala
			20					25					30		

Val Ala Val Ala Met Gly Met Gly Pro Ala Phe Ala Pro Lys Val Ala
 35 40 45

Glu Ala
 50

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Asn Arg Arg Asn Phe Ile Lys Ala Ala Ser Cys Gly Ala Leu Leu
 1 5 10 15

Thr Gly Ala Leu Pro Ser Val Ser His Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Ser His Ala Asp Glu His Ala Gly Asp His Gly Ala Thr Arg Arg
 1 5 10 15

Asp Phe Leu Tyr Tyr Ala Thr Ala Gly Ala Gly Thr Val Ala Ala Gly
 20 25 30

Ala Ala Ala Trp Thr Leu Val Asn Gln Met Asn Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Thr Gln Ile Ser Gly Ser Pro Asp Val Pro Asp Leu Gly Arg Arg
 1 5 10 15

Gln Phe Met Asn Leu Leu Thr Phe Gly Thr Ile Thr Gly Val Ala Ala
 20 25 30

Gly Ala Leu Tyr Pro Ala Val Lys Tyr Leu Ile Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Asp Arg Arg Thr Phe Leu Arg Leu Tyr Leu Leu Val Gly Ala Ala
 1 5 10 15
 Ile Ala Val Ala Pro Val Ile Lys Pro Ala Leu Asp Tyr Val Gly Tyr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Thr Lys Leu Ser Gly Gln Glu Leu His Ala Glu Leu Ser Arg Arg
 1 5 10 15
 Ala Phe Leu Ser Tyr Thr Ala Ala Val Gly Ala Leu Gly Leu Cys Gly
 20 25 30
 Thr Ser Leu Leu Ala Gln Gly Ala Arg Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Leu Thr Arg Arg Glu Phe Ile Lys His Ser Gly Ile Ala Ala
 1 5 10 15
 Gly Ala Leu Val Val Thr Ser Ala Ala Pro Leu Pro Ala Trp Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Thr	Ile	Ser	Arg	Arg	Asp	Leu	Leu	Lys	Ala	Gln	Ala	Ala	Gly	Ile
1				5					10					15	
Ala	Ala	Met	Ala	Ala	Asn	Ile	Pro	Leu	Ser	Ser	Gln	Ala	Pro	Ala	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ser	Glu	Ala	Leu	Ser	Gly	Arg	Gly	Asn	Asp	Arg	Arg	Lys	Phe	Leu
1				5					10					15	
Lys	Met	Ser	Ala	Leu	Ala	Gly	Val	Ala	Gly	Val	Ser	Gln	Ala	Val	Gly
				20				25					30		

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Lys	Thr	Lys	Ile	Pro	Asp	Ala	Val	Leu	Ala	Ala	Glu	Val	Ser	Arg
1				5					10					15	
Arg	Gly	Leu	Val	Lys	Thr	Thr	Ala	Ile	Gly	Gly	Leu	Ala	Met	Ala	Ser
			20					25					30		
Ser	Ala	Leu	Thr	Leu	Pro	Phe	Ser	Arg	Ile	Ala	His	Ala			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ser Asn Phe Asn Gln Ile Ser Arg Arg Asp Phe Val Lys Ala Ser
1 5 10 15
Ser Ala Gly Ala Ala Leu Ala Val Ser Asn Leu Thr Leu Pro Phe Asn
20 25 30
Val Met Ala
35

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ser Ile Ser Arg Arg Ser Phe Leu Gln Gly Val Gly Ile Gly Cys
1 5 10 15
Ser Ala Cys Ala Leu Gly Ala Phe Pro Pro Gly Ala Leu Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Lys Thr Val Leu Pro Ser Val Pro Glu Thr Val Arg Leu Ser Arg
1 5 10 15
Arg Gly Phe Leu Val Gln Ala Gly Thr Ile Thr Cys Ser Val Ala Phe
20 25 30
Gly Ser Val Pro Ala
35

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Arg Leu Asn Arg Phe Arg Leu Gly Lys Asp Gly Arg Arg Glu
1 5 10 15
Gln Ala Ser Leu Ser Arg Arg Gly Phe Leu Val Thr Ser Leu Gly Ala
20 25 30
Gly Val Met Phe Gly Phe Ala Arg Pro Ser Ser Ala
35 40

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Ser Asp Lys Asp Ser Lys Asn Thr Pro Gln Val Pro Glu Lys Leu
1 5 10 15
Gly Leu Ser Arg Arg Gly Phe Leu Gly Ala Ser Ala Val Thr Gly Ala
20 25 30
Ala Val Ala Ala Thr Ala Leu Gly Gly Ala Val Met Thr Arg Glu Ser
35 40 45
Trp Ala
50

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Glu Ser Arg Thr Ser Arg Arg Thr Phe Val Lys Gly Leu Ala Ala
1 5 10 15
Ala Gly Val Leu Gly Gly Leu Gly Leu Trp Arg Ser Pro Ser Trp Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ser Leu Ser Arg Arg Gln Phe Ile Gln Ala Ser Gly Ile Ala Leu
1 5 10 15
Cys Ala Gly Ala Val Pro Leu Lys Ala Ser Ala
20 25

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Leu Gly Lys Ser Gln Phe Asp Asp Leu Phe Glu Lys Met Ser Arg
1 5 10 15
Lys Val Ala Gly His Thr Ser Arg Arg Gly Phe Ile Gly Arg Val Gly
20 25 30
Thr Ala Val Ala Gly Val Ala Leu Val Pro Leu Leu Pro Val Asp Arg
35 40 45
Arg Gly Arg Val Ser Arg Ala Asn Ala
50 55

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Thr Leu Asn Arg Arg Asp Phe Ile Lys Thr Ser Gly Ala Ala Val
1 5 10 15
Ala Ala Val Gly Ile Leu Gly Phe Pro His Leu Ala Phe Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met	Thr	Asp	Ser	Arg	Ala	Asn	Arg	Ala	Asp	Ala	Thr	Arg	Gly	Val	Ala
1				5					10					15	
Ser	Val	Ser	Arg	Arg	Arg	Phe	Leu	Ala	Gly	Ala	Gly	Leu	Thr	Ala	Gly
			20					25					30		
Ala	Ile	Ala	Leu	Ser	Ser	Met	Ser	Thr	Ser	Ala	Ser	Ala			
		35					40					45			